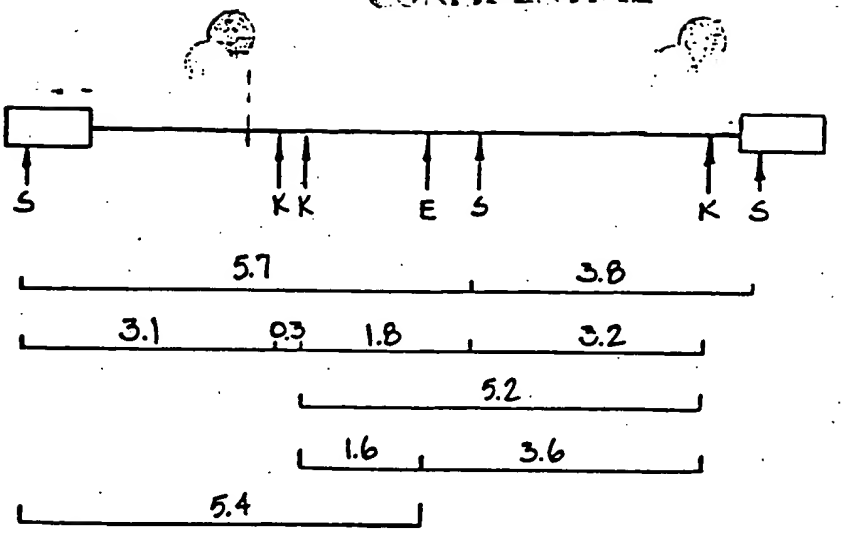

FIG. 1.

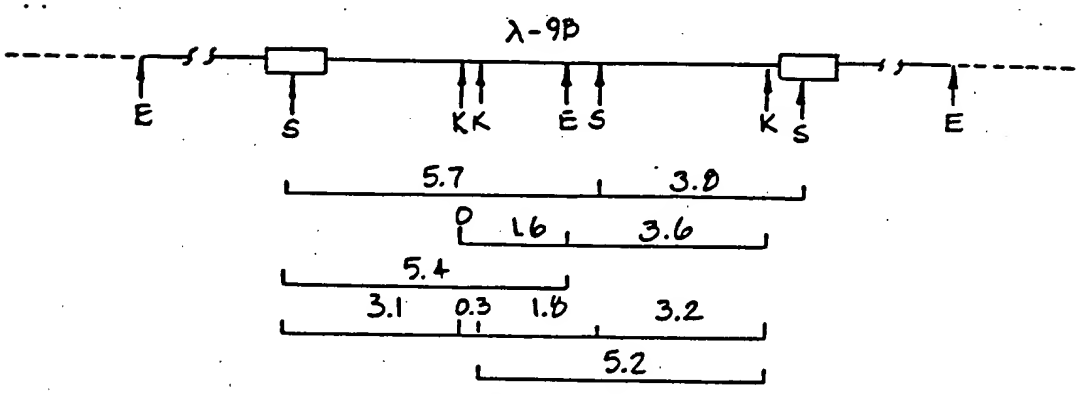

FIG. 2.

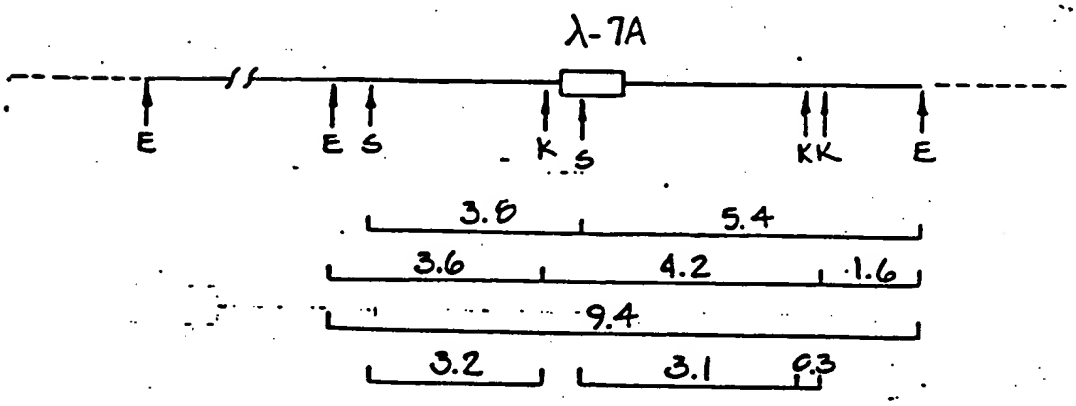

FIG. 3.

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Argument Map in DNA Strand scarv2
from the '/v/lib/6mers' file.
Translation shown at open reading frames.

FIGURE 4
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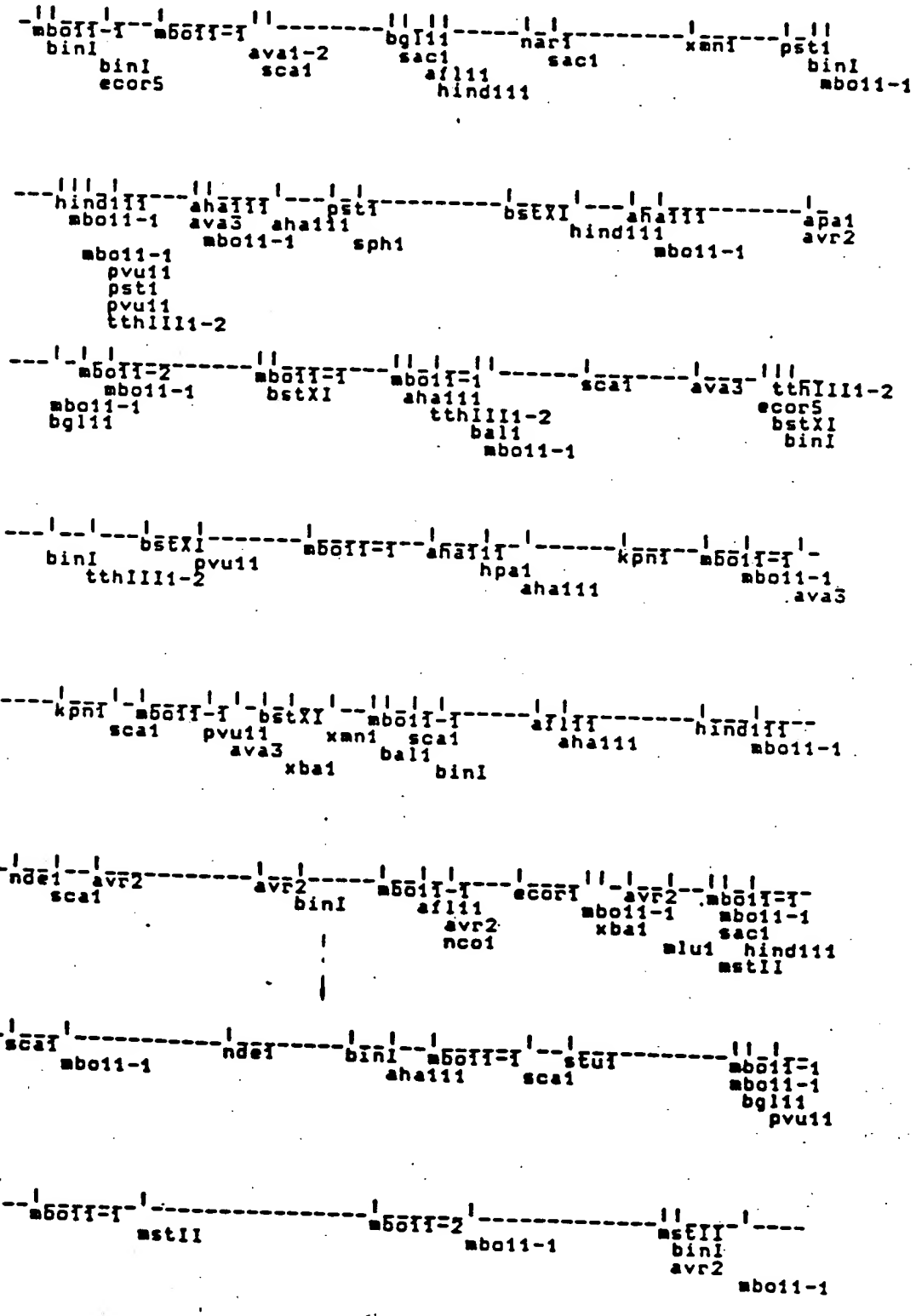

Figure 4
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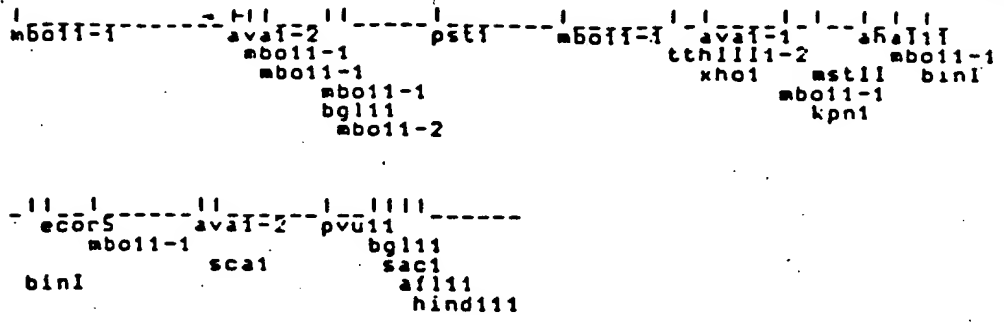


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   1  CTGGAAGGGCTAATTTGGTCCCAAAGAAGACAAGAGATCCTTGATCTGTGGATCTACCACAC
      GACCTTCCCGATTAAACCAGGGTTTCTTCTGTTCTCTAGGAACTAGACACCTAGATGGTGTG

      26 mbo11, 50 binI,

  63  ACAAGGCTACTTCCCTGATTGGCAGAATTACACACCAGGGCCAGGGATCAGATATCCACT
      TGTTCCGATGAAGGGACTAACCGTCTTAATGTGTGGTCCCGGTCCCTAGTCTATAGGTGA

      107 binI, 113 ecor5,

 123  GACCTTTGGATGGTGCTTCAAGCTAGTACCAGTTGAGCCAGAGAAGGTAGAAGAGGCCAA
      CTGGAAACCTACCACGAAGTTCGATCATGGTCAACTCGGTCTCTTCCATCTTCTCCGGTT

      172 mbo11,

 183  TGAAGGAGAGAACAACAGCTTGTTACACCCTATGAGCCTGCATGGGATGGAGGACGCGGA
      ACTTCCTCTCTTGTTGTCGAACAATGTGGGATACTCGGACGTACCCTACCTCCTGCGCCT

 243  GAAAGAAGTGTTAGTGTGGAGGTTTGACAGCAAACTAGCATTTCATCACATGGCCCGAGA
      CTTTCTTCACAATCACACCTCCAAACTGTCGTTTGATCGTAAAGTAGTGTACCGGGCTCT

      296 aval,

 303  GCTGCATCCGGAGTACTACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACTTTCCGC
      CGACGTAGGCCTCATGATGTTTCTGACGACTGTAGCTCGAAAGATGTTCCCTGAAAGGCG

      314 sca1,

 363  TGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGTCCCTCAGATGC
      ACCCCTGAAAGGTCCCTCCGCACCGGACCCGCCCTGACCCCTCACCGCAGGGAGTCTACG

 423  TGCATATAAGCAGACTGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAG
      ACGTATATTCGTCTGACGAAAAACGGACATGACCCAGAGAGACCAATCTGGTCTAGACTC

      474 bgl11,

 483  CCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTT
      GGACCCTCGAGAGACCGATTGATCCCTTGGGTGACGAATTCGGAGTTATTTCGAACGGAA

      488 sac1, 518 afl11, 532 hind111,

 543  GAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCA
      CTCACGAAGTTCATCACACACGGGCAGACAACACACTGAGACCATTGATCTCTAGGGAGT

 603  GACCCTTTTAGTCAGTGTGGAAAAATCTCTAGCAGTGGCGCCCGAACAGGGACGCGAAAG
      CTGGGAAAATCAGTCACACCTTTTTAGAGATCGTCACCGCGGGCTTGTCCCTGCGCTTTC

      639 nar1,

 663  CGAAAGTAGAACCAGAGGAGCTCTCTCGACGCAGGACTCGGCTTGCTGAAGCGCGCACAG
      GCTTTCATCTTGGTCTCCTCGAGAGAGCTGCGTCCTGAGCCGAACGACTTCGCGCGTGTC

      680 sac1,

 723  CAAGAGGCGAGGGGCGGCGACTGGTGAGTACGCCAATTTTTGACTAGCGGAGGCTAGAAG
      GTTCTCCGCTCCCCGCCGCTGACCACTCATGCGGTTAAAAACTGATCGCCTCCGATCTTC

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 783  GAGAGAGAGATGGGTGCGAGAGCGTCGGTATTAAGCGGGGGAGAATTAGATAAATGGGAA
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      TTTTAAGCCAATTCCGGTCCCCCTTTCTTTTTTATATTCAATTTTGTATATCATACCCGT

 903  SerArgGluLeuGluArgPheAlaValAsnProGlyLeuLeuGluThrSerGluGlyCys
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      TCGTCCCTCGATCTTGCTAAGCGTCAGTTAGGACCGGACAATCTTTGTAGTCTTCCGACG

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 963  ArgGlnIleLeuGlyGlnLeuGlnProSerLeuGlnThrGlySerGluGluLeuArgSer
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      1002 binI, 1008 mbo11,

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      AATATATTATGTCATCGTTGGGAGATAACACATGTAGTTTCCTATCTACATTTTCTGTGG

1083  LysGluAlaLeuGluLysIleGluGluGluGlnAsnLysSerLysLysLysAlaGlnGln
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      TTCCTTCGAAATCTCTTCTATCTCCTTCTCGTTTTGTTTTCATTCTTTTTCCGTGTCGTT

      1087 hind111, 1097 mbo11, 1107 mbo11,

1143  AlaAlaAlaAlaAlaGlyThrGlyAsnSerSerGlnValSerGlnAsnTyrProIleVal
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      CGTCGTCGACGTCGACCGTGTCCTTTGTCGTCGGTCCAGTCGGTTTTAATGGGATATCAC

      1147 pvu11, 1150 pst1, 1153 pvu11, 1156 tthIII1,

1203  GlnAsnLeuGlnGlyGlnMetValHisGlnAlaIleSerProArgThrLeuAsnAlaTrp
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      GTCTTGGATGTCCCCGTTTACCATGTAGTCCGGTATAGTGGATCTTGAAATTTACGTACC

      1250 aha111, 1255 ava3,

1263  ValLysValValGluGluLysAlaPheSerProGluValIleProMetPheSerAlaLeu
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      CATTTTCATCATCTTCTTTTCCGAAAGTCGGGTCTTCATTATGGGTACAAAAGTCGTAAT

      1275 mbo11,

1323  SerGluGlyAlaThrProGlnAspLeuAsnThrMetLeuAsnThrValGlyGlyHisGln
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      AGTCTTCCTCGGTGGGGTGTTCTAAATTTGTGGTACGATTTGTGTCACCCCCCTGTAGTT

      1346 aha111,

1383  AlaAlaMetGlnMetLeuLysGluThrIleAsnGluGluAlaAlaGluTrpAspArgVal
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      CGTCGGTACGTTTACAATTTTCTCTGATAGTTACTCCTTCGACGTCTTACCCTATCTCAC

      1423 pst1,

1443  HisProValHisAlaGlyProIleAlaProGlyGlnMetArgGluProArgGlySerAsp
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      GTAGGTCACGTACGTCCCGGATAACGTGGTCCGGTTTACTCTCTTGGTTCCCCTTCACTG

      1451 sph1,

1503  IleAlaGlyThrThrSerThrLeuGlnGluGlnIleGlyTrpMetThrAsnAsnProPro
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      TATCGTCCTTGATGATCATGGGAAGTCCTTGTTTATCCTACCTACTGTTTATTAGGTGGA

1563  IleProValGlyGluIleTyrLysArgTrpIleIleLeuGlyLeuAsnLysIleValArg
      ATCCCAGTAGGAGAAATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAGTAAGA
      TAGGGTCATCCTCTTTAGATATTTTCTACCTATTAGGACCCTAATTTATTTTATCATTCT

1623  MetTyrSerProThrSerIleLeuAspIleArgGlnGlyProLysGluProPheArgAsp
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      TACATATCGGGATGGTCGTAAGACCTGTATTCTGTTCCTGGTTTCCTTGGGAAATCTCTA

      1636 bstXI,

1683  TyrValAspArgPheTyrLysThrLeuArgAlaGluGlnAlaSerGlnAspValLysAsn
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      ATACATCTGGCCAAGATATTTTGAGATTCTCGGCTTGTTCGAAGTGTCCTACATTTTTTA

      1720 hind111,
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                ACCTACTGTCTTTGGAACAACCAGGTTTTACGTTTGGGTCTAACATTCTGATAAAATTTT

                1796 aha111,

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1803            GCATTGGGACCAGCAGCTACACTAGAAGAAATGATGACAGCATGTCAGGGAGTGGGGGGA
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1923            ATAATGATGCAGAGAGGCAATTTTAGGAACCAAAGAAAGACTGTTAAGTGTTTCAATTGT
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                GlyLysGluGlyHisIleAlaLysAsnCysArgAlaProArgLysLysGlyCysTrpArg
1983            GGCAAAGAAGGGCACATAGCCAAAAATTGCAGGGCCCCTAGGAAAAAGGGCTGTTGGAGA
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                2014 apa1, 2019 avr2,

                CysGlyArgGluGlyHisGlnMetLysAspCysThrGluArgGlnAlaAsnPheLeuGly
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                ACACCTTCCCTTCCTGTGGTTTACTTTCTAACGTGACTCTCTGTCCGATTAAAAAATCCC

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2103            AAGATCTGGCCTTCCTACAAGGGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAGAGCCA
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2163            ACAGCCCCACCAGAAGAGAGCTTCAGGTTTGGGGAGGAGAAAACAACTCCCTCTCAGAAG
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                2175 mbo11,

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2223            CAGGAGCCGATAGACAAGGAACTGTATCCTTTAACTTCCCTCAGATCACTCTTTGGCAAC
                GTCCTCGGCTATCTGTTCCTTGACATAGGAAATTGAAGGGAGTCTAGTGAGAAACCGTTG

                AspProSerSerGlnOC
2283            GACCCCTCGTCACAATAAGGATAGGGGGGCAACTAAAGGAAGCTCTATTAGATACAGGA
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2342            GCAGATGATACAGTATTAGAAGAAATGAATTTGCCAGGAAAATGGAAACCAAAAATGATA
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                GlyGlyIleGlyGlyPheIleLysValArgGlnTyrAspGlnIleProValGluIleCys
2402            GGGGGAATTGGAGGTTTTATCAAAGTAAGACAGTACGATCAGATACCTGTAGAAATCTGT
                CCCCCTTAACCTCCAAAATAGTTTCATTCTGTCATGCTAGTCTATGGACATCTTTAGACA

                GlyHisLysAlaIleGlyThrValLeuValGlyProThrProValAsnIleIleGlyArg
2462            GGACATAAAGCTATAGGTACAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGA
                CCTGTATTTCGATATCCATGTCATAATCATCCTGGATGTGGACAGTTGTATTAACCTTCT

                2517 mbo11,

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                TTAGACAACTGAGTCTAACCAACATGAAATTTAAAGGGGTAATCAGGATAACTTTGACAT

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                ProValLysLeuLysProGlyMetAspGlyProLysValLysGlnTrpProLeuThrGlu
2582            CCAGTAAAATTAAAGCCAGGAATGGATGGCCCAAAAGTTAAGCAATGGCCATTGACAGAA
                GGTCATTTTAATTTCGGTCCTTACCTACCGGGTTTTCAATTCGTTACCGGTAACTGTCTT

                2627 ba11, 2639 mbo11,

                GluLysIleLysAlaLeuValGluIleCysThrGluMetGluLysGluGlyLysIleSer
2642            GAAAAAATAAAAGCATTAGTAGAGATATGTACAGAAATGGAAAAGGAAGGGAAAATTTCA
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Figure 4
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2702            AAAATTGGGCCTGAAAATCCATACAATACTCCAGTATTTGCTATAAAGAAAAAAGACAGT
                TTTTAACCCGGACTTTTAGGTATGTTATGAGGTCATAAACGATATTTCTTTTTTCTGTCA

                2759 sca1,

                ThrLysTrpArgLysLeuValAspPheArgGluLeuAsnLysArgThrGlnAspPheTrp
2762            ACTAAATGGAGAAAACTAGTAGATTTCAGAGAACTTAATAAAAGAACTCAAGACTTCTGG
                TGATTTACCTCTTTTGATCATCTAAAGTCTCTTGAATTATTTTCTTGAGTTCTGAAGACC

                GluValGlnLeuGlyIleProHisProGlyOC
2822            GAAGTTCAGTTAGGAATACCACACCCGCAGGGTTAAAAAAAAGAAAAAATCAGTAACAGTA
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2882            TTGGATGTGGGTGATGCATACTTTTCAGTTCCCTTAGATAAAGACTTTAGAAAGTATACTG
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                2895 ava3,

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2943            CATTTACCATACCTAGTATAAACAATGAGACACCAGGGATTAGATATCAGTACAATGTGG
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                2985 ecor5,

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3003            CTGCCACAGGGATGGAAAGGATCACCAGCAATATTCCAAAGTAGCATGACAAAAATCTTA
                GACGGTGTCCCTACCTTTCCTAGTGGTCGTTATAAGGTTTCATCGTACTGTTTTTAGAAT

                3003 tthIII1, 3006 bstXI, 3021 binI,

                GluProPheArgLysGlnAsnProAspIleValIleTyrGlnTyrMetAspAspLeuTyr
3063            GAGCCTTTTAGAAAACAGAATCCAGACATAGTTATCTATCAATACATGGATGATTTGTAT
                CTCGGAAAATCTTTTGTCTTAGGTCTGTATCAATAGATAGTTATGTACCTACTAAACATA

                ValGlySerAspLeuGluIleGlyGlnHisArgThrLysIleGluGluLeuArgGlnHis
3123            GTAGGATCTGACTTAGAAATAGGGCAGCATAGAACAAAAATAGAGGAACTGAGACAGCAT
                CATCCTAGACTGAATCTTTATCCCGTCGTATCTTGTTTTTATCTCCTTGACTCTGTCGTA

                3126 binI, 3171 tthIII1,

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                GACAACTCCACCCCTAAATGGTGTGGTCTGTTTTTTGTAGTCTTTCTTGGAGGTAAGGAA

                3234 bstXI,

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3243            TGGATGGGTTATGAACTCCATCCTGATAAATGGACAGTACAGCCTATAATGCTGCCAGAA
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                3308 pvu11,

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3423            CTAACAGAAGTAATACCACTAACAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGGGAG
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                3447 mbo11,

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3543            ATACAGAAGCAGGGGCAAGGCCAATGGACATATCAAATTTATCAAGAGCCATTTAAAAAT
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                3594 aha111,

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3603            CTGAAAACAGGAAAGTATGCAAGGATGAGGGGTGCCCACACTAATGATGTAAAACAGTTA
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                3659 hpa1,
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                3723 aha111,

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3783            ACCTGGATTCCTGAGTGGGAGTTTGTCAATACCCCTCCCTTAGTGAAATTATGGTACCAG
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                3835 kpn1,

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3903            GAGACTAAATTAGGAAAAGCAGGATATGTTACTGACAGAGGAAGACAAAAAGTTGTCTCC
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                4060 ava3,

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4083            CAACCAGATAAGAGTGAATCAGAGTTAGTCAGTCAAATAATAGAGCAGTTAATAAAAAAG
                GTTGGTCTATTCTCACTTAGTCTCAATCAGTCAGTTTATTATCTCGTCAATTATTTTTTC

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4143            GAAAAGGTCTACCTGGCATGGGTACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTA
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4323            CCACCTGTAGTAGCAAAAGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAA
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                4497 xmn1,

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                4605 sca1,

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4623            GCCTGTTGGTGGGCAGGGATCAAGCAGGAATTTGGCATTCCCTACAATCCCCAAAGTCAA
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                4639 binI,

                GlyValValGluSerMetAsnAsnGluLeuLysLysIleIleGlyGlnValArgAspGln
4683            GGAGTAGTAGAATCTATGAATAATGAATTAAAGAAAATTATAGGACAGGTAAGAGATCAG
                CCTCATCATCTTAGATACTTATTACTTAATTTCTTTTAATATCCTGTCCATTCTCTAGTC

                AlaGluHisLeuLysThrAlaValGlnMetAlaValPheIleHisAsnPheLysArgLys
4743            GCTGAACACCTTAAGACAGCAGTACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAA
                CGACTTGTGGAATTCTGTCGTCATGTTTACCGTCATAAGTAGGTGTTAAAATTTTCTTTT

                4752 af111, 4791 aha111,

                GlyGlyIleGlyGlyTyrSerAlaGlyGluArgIleValAspIleIleAlaThrAspIle
4803            GGGGGGATTGGGGGATACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATA
                CCCCCCTAACCCCCTATGTCACGTCCCCTTTCTTATCATCTGTATTATCGTTGTCTGTAT

                GlnThrLysGluLeuGlnLysGlnIleThrLysIleGlnAsnPheArgValTyrTyrArg
4863            CAAACTAAAGAACTACAAAAGCAAATTACAAAAATTCAAAATTTTCGGGTTTATTACAGG
                GTTTGATTTCTTGATGTTTTCGTTTAATGTTTTTAAGTTTTAAAAGCCCAAATAATGTCC

                AspAsnLysAspProLeuTrpLysGlyProAlaLysLeuLeuTrpLysGlyGluGlyAla
4923            GACAACAAAGATCCCCTTTGGAAAGGACCAGCAAAGCTTCTCTGGAAAGGTGAAGGGGCA
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                4956 hind111,

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                5023 mbo11,

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5043            AGGGATTATGGAAAACAGATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGAT
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                AM
5103            TAGAACATGGAAAAGTTTAGTAAAACACCATATGTATATTTCAAAGAAAGCTAAAGGATGG
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                5185 sca1,

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5221            CCCCTAGGGGATGCTAAATTGGTAATAACAACATATTGGGGTCTGCATACAGGAGAAAGA
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5281            GAATGGCATTTGGGTCAGGGAGTCGCCATAGAATGGAGGAAAAAGAAATATAGCACACAA
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5341            GTAGACCCTGGCCTAGCAGACCAACTAATTCATCTGCATTATTTTGATTGTTTTCAGAA
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                GlnLysThrLysGlyHisArgGlySerHisThrMetAsnGlyHisAM
5581            CAGAAGACCAAGGGCCACAGAGGGAGCCATACAATGAATGGACACTAGAGCTTTTAGAGG
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                5583 mbo11,

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                5643 af111, 5670 avr2, 5676 nco1,

5701            ATATCTATGAAACTTATGGGGATACTTGGGCAGGAGTGGAAGCCATAATAAGAATTCTGC
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                5752 ecor1,

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5821            AACAGAGGAGAGCAAGAAGAAATGGAGCCAGTAGATCCTAATCTAGAGCCCTGGAAGCAT
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                5836 mbo11, 5862 xba1,

5881            CCAGGAAGTCAGCCTAGGACTGCTTGTAACAATTGCTATTGTAAAAAGTGTTGCTTTCAT
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                5893 avr2,

5941            TGCTACGCGTGTTTCACAAGAAAAGGCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGA
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                5945 mlu1, 5988 mbo11,

6001            CAGCGACGAAGAGCTCCTCAGGACAGTCAGACTCATCAAGCTTCTCTATCAAAGCAGTAA
                GTCGCTGCTTCTCGAGGAGTCCTGTCAGTCTGAGTAGTTCGAAGAGATAGTTTCGTCATT

                6008 mbo11, 6011 sac1, 6016 mstII, 6038 hind111,

6061            GTAGTAAATGTAATGCAATCTTTACAAATATTAGCAATAGTATCATTAGTAGTAGTAGCA
                CATCATTTACATTACGTTAGAAATGTTTATAATCGTTATCATAGTAATCATCATCATCGT

6121            ATAATAGCAATAGTTGTGTGGACCATAGTACTCATAGAATATAGGAAAATATTAAGACAA
                TATTATCGTTATCAACACACCTGGTATCATGAGTATCTTATATCCTTTTATAATTCTGTT

                6147 sca1,

                                                                    MetLys  ENV
6181            AGAAAATAGACAGATTAATTGATAGAATAAGAGAAAAAGCAGAAGACAGTGGCAATGAAA
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                6222 mbo11,

6241            ValLysGlyThrArgArgAsnTyrGlnHisLeuTrpArgTrpGlyThrLeuLeuLeuGly
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                CACTTCCCCTGGTCCTCCTTAATAGTCGTGAACACCTCTACCCCGTGGAACGAGGAACCC

6301            MetLeuMetIleCysSerAlaThrGluLysLeuTrpValThrValTyrTyrGlyValPro
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                TACAACTACTAGACATCACGATGTCTTTTTAACACCCAGTGTCAAATAATACCTCATGGA

6361            ValTrpLysGluAlaThrThrThrLeuPheCysAlaSerAspAlaArgAlaTyrAspThr
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                6410 nde1,

6421            GluValHisAsnValTrpAlaThrHisAlaCysValProThrAspProAsnProGlnGlu
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                CTCCATGTATTACAAACCCGGTGTGTACGGACACATGGGTGTCTGGGGTTGGGTGTTCTT

6481            ValValLeuGlyAsnValThrGluAsnPheAsnMetTrpLysAsnAsnMetValGluGln
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                CATCATAACCCTTTACACTGTCTTTTAAAATTGTACACCTTTTTATTGTACCATCTTGTC

6541            MetGlnGluAspIleIleSerLeuTrpAspGlnSerLeuLysProCysValLysLeuThr
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                6615 aha111,

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                6790 sca1,

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                6851 stu1,

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7021            CTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGACAATTTCACGAAC
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                7042 mbo11, 7045 mbo11, 7060 bgl11,

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                7102 pvu11,

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7141            AACAACAATACAAGAAAAAGTATCTATATAGGACCAGGGAGAGCATTTCATACAACAGGA
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                7199 mbo11,

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7261            ACTTTAGAACAGATAGTTAAAAAATTAAGAGAACAGTTTGGGAATAATAAAACAATAGTC
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7321            TTTAATCAATCCTCAGGAGGGGACCCAGAAATTGTAATGCACAGTTTTAATTGTAGAGGG
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                7331 mstII,

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7381            GAATTTTTCTACTGTAATACAACACAACTGTTTAATAATACATGGAGGTTAAATCACACT
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7441            GAAGGAACTAAAGGAAATGACACAATCATACTCCCATGTAGAATAAAACAAATTATAAAC
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                7736 mbo11,

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7801            GGAGCAGCAGGAAGCACTATGGGCGCAGTGTCATTGACGCTGACGGTACAGGCCAGACAA
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7861            TTATTGTCTGGTATAGTGCAACAGCAGAACAATTTGCTGAGGGCTATTGAGGCGCAACAA
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7921            CATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAGCTCCAGGCAAGAGTCCTGGCTGTG
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7981            GAAAGATACCTAAGGGATCAACAGCTCCTAGGGATTTGGGGTTGCTCTGGAAAACTCATT
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                7989 mstII, 7995 binI, 8007 avr2,

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8041            TGCACCACTGCTGTGCCTTGGAATGCTAGTTGGAGTAATAAATCTCTGGAAGACATTTGG
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                8089 mbo11,

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                8170 mbo11,

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8221            GATAAGTGGGCAAGTTTGTGGAATTGGTTTAGCATAACAAACTGGCTGTGGTATATAAAG
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8281            ATATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTGCTTTCT
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8341            ATAGTGAATAGAGTTAGGCAGGGATACTCACCATTGTCATTTCAGACCCGCCTCCCAGTC
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                8400 ava1,

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8401            CCGAGGGGACCCGACAGGCCCGATGGAATCGAAGAAGAAGGTGGAGAGAGAGACAGAGAC
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                8431 mbo11, 8434 mbo11,

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                8503 mbo11, 8505 bglii,

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8521            TGCCTCTTCAGCTACCGCCGCTTGAGAGACTTACTCTTGATTGCAGCGAGGACTGTGGAA
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                8525 mbo11,
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                8629 pst1,

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8701            GAGGGGACAGATAGGGTTATAGAAGTAGCACAAAGAGCTTATAGAGCTATTCTCCACATA
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8761            CATAGAAGAATTAGACAGGGCTTGGAAAGGCTTTTGCTATAAGATGGGTGGCAAGTGGTCA
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8882            GCTGAGCCAGCAGCAGATGGGGTGGGAGCAGTATCTCGAGACCTGGAAAAACATGGAGCA
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                8883 tthIII1, 8916 ava1 xho1,

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8942            ATCACAAGTAGCAATACAGCAGCTACTAATGCTGATTGTGCCTGGCTAGAAGCACAAGAG
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9002            GAGGAAGAGGTGGGTTTTCCAGTCAGACCTCAGGTACCTTTAAGACCAATGACTTACAAG
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                9005 mbo11, 9029 mstII, 9034 kpn1,

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9062            GCAGCTTTAGATATTAGCCACTTTTTAAAAGAAAAGGGGGGACTGGAAGGGCTAATTTGG
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                9085 aha111,

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9122            TCCCAAAGAAGACAAGAGATCCTTGATCTGTGGATCTACCACACACAAGGCTACTTCCCT
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                9129 mbo11, 9153 binI,

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9182            GATTGGCAGAATTACACACCAGGGCCAGGGATCAGATATCCACTGACCTTTGGATGGTGC
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                9210 binI, 9216 ecor5,

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9242            TTCAAGCTAGTACCAGTTGAGCCAGAGAAGGTAGAAGAGGCCAATGAAGGAGAGAACAAC
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                9275 mbo11,

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9302            AGCTTGTTACACCCTATGAGCCTGCATGGGATGGAGGACGCGGAGAAAGAAGTGTTAGTG
                TCGAACAATGTGGGATACTCGGACGTACCCTACCTCCTGCGCCTCTTTCTTCACAATCAC

                TrpArgPheAspSerLysLeuAlaPheHisHisMetAlaArgGluLeuHisProGluTyr
9362            TGGAGGTTTGACAGCAAACTAGCATTTCATCACATGGCCCGAGAGCTGCATCCGGAGTAC
                ACCTCCAAACTGTCGTTTGATCGTAAAGTAGTGTACCGGGCTCTCGACGTAGGCCTCATG

                9399 ava1, 9417 sca1,

                TyrLysAspCysOP
9422            TACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACTTTCCGCTGGGGACTTTCCAGGG
                ATGTTTCTGACGACTGTAGCTCGAAAGATGTTCCCTGAAAGGCGACCCCTGAAAGGTCCC

9482            AGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGTCCCTCAGATGCTGCATATAAGCAGCTG
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                9536 pvu11,
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Figure 4
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```
9542  CTTTTTGCCTGTACTGGGTCTC  GGTTAGACCAGATCTGAGCCTGGGAGC TCTGGC
      GAAAAACGGACATGACCCAGAGAGACCAATCTGGTCTAGACTCGGACCCTCGAGAGACCG

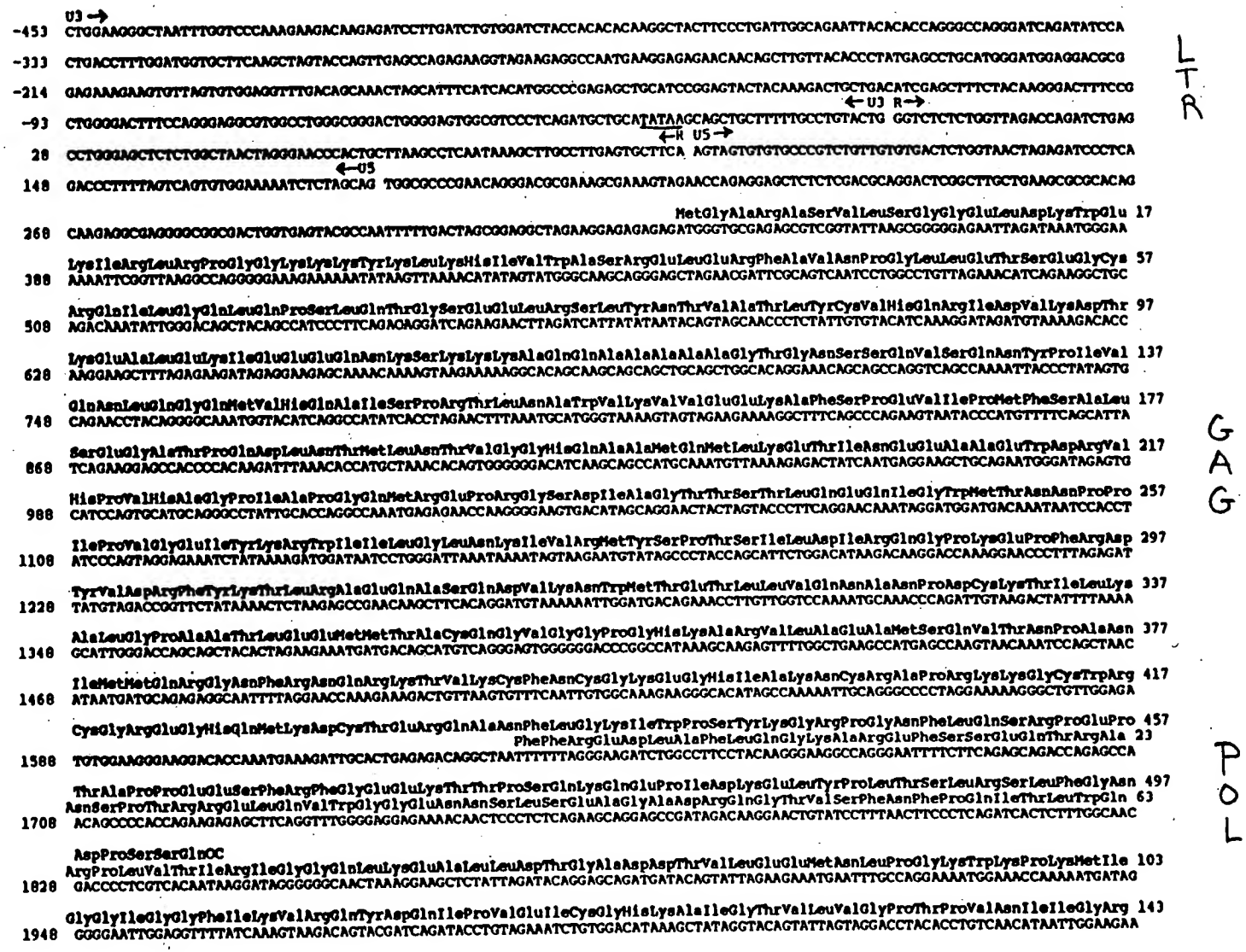
      9576 bglii, 9590 sacI,

9602  TAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAGTGCTTCAAGTAGTG
      ATTGATCCCTTGGGTGACGAATTCGGAGTTATTTCGAACGGAACTCACGAAGTTCATCAC

      9620 afIII, 9634 hindIII,

9662  TGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGACCCTTTTAGTCAGTG
      ACACGGGCAGACAACACACTGAGACCATTGATCTCTAGGGAGTCTGGGAAAATCAGTCAC

9722  TGGAAAAATCTCTAGCAG
      ACCTTTTTAGAGATCGTC
```



LTR

GAG

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FIGURE 5
1 of 4

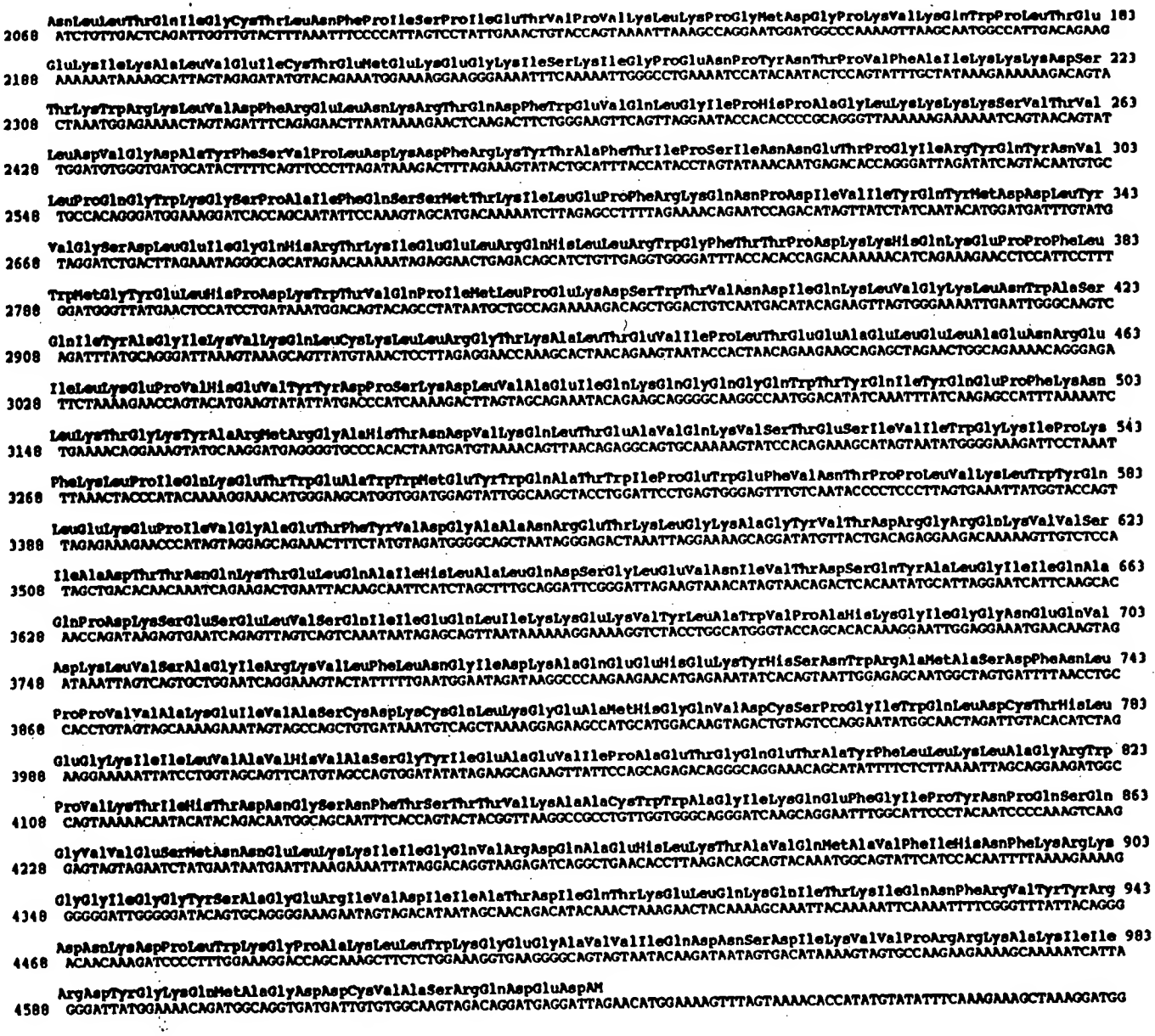

FIGURE 5
2 of 4

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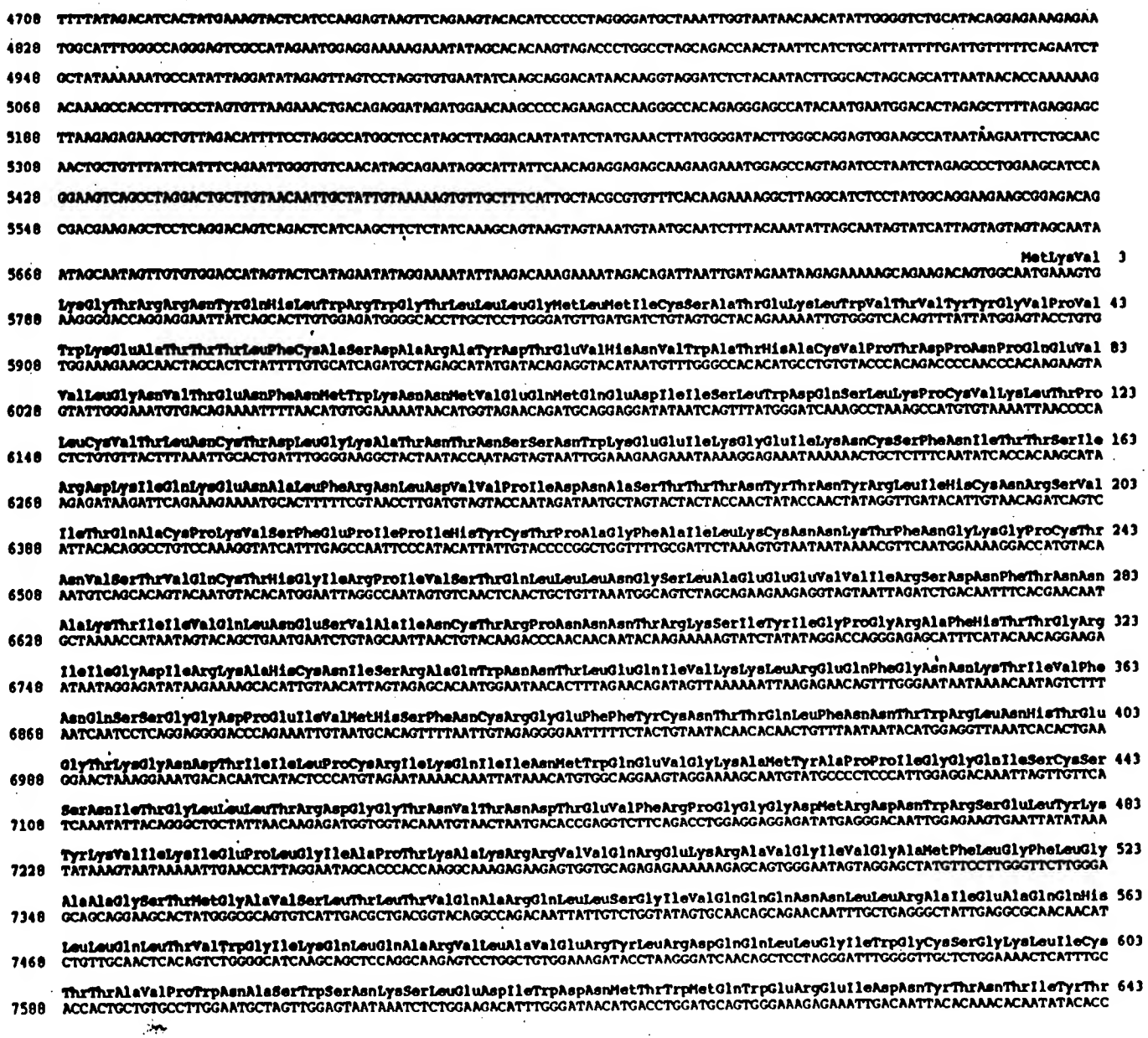


FIGURE 5
3 of 4

FIGURE 5
4 of 4

ENV

LTR

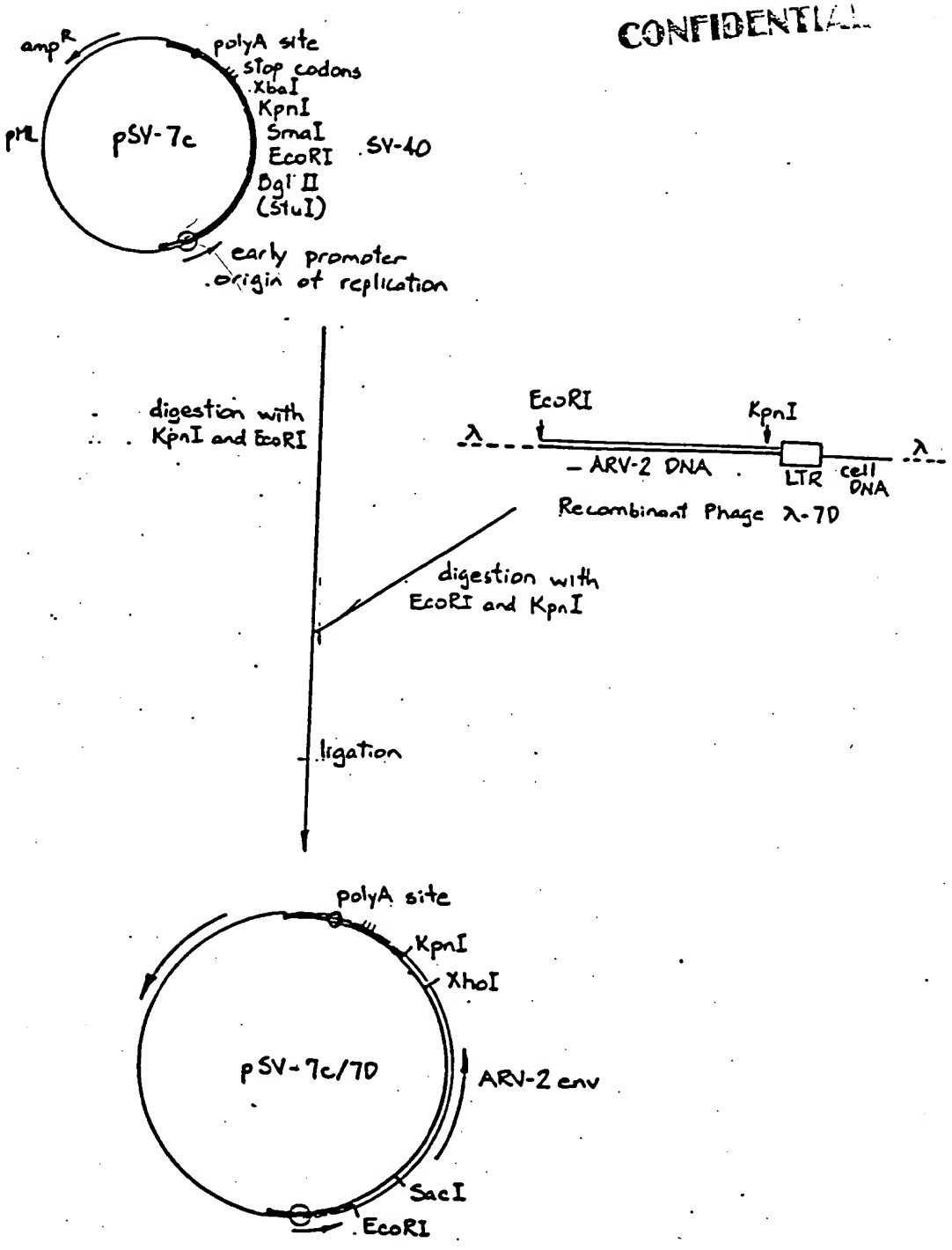


FIG. 6

Figure 7

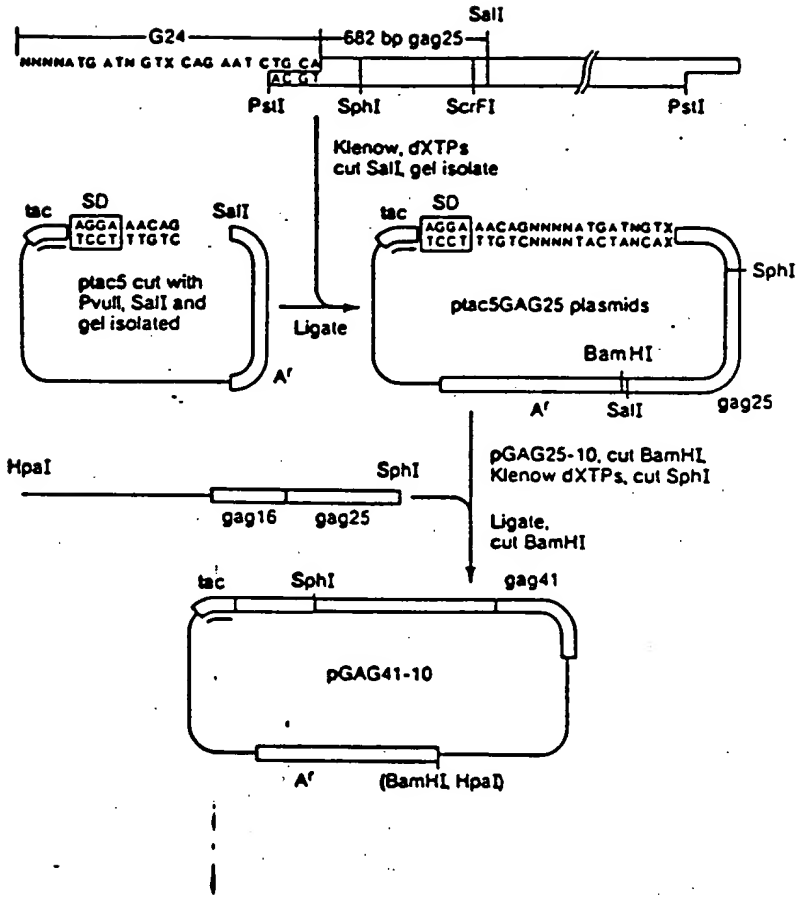


FIG. 8

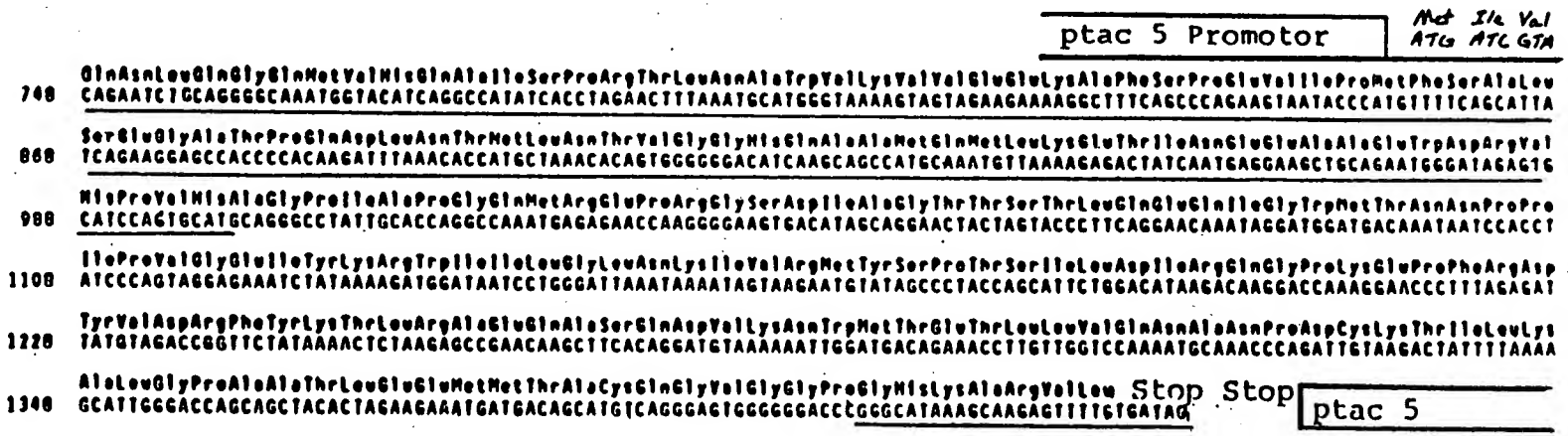


FIG. 9

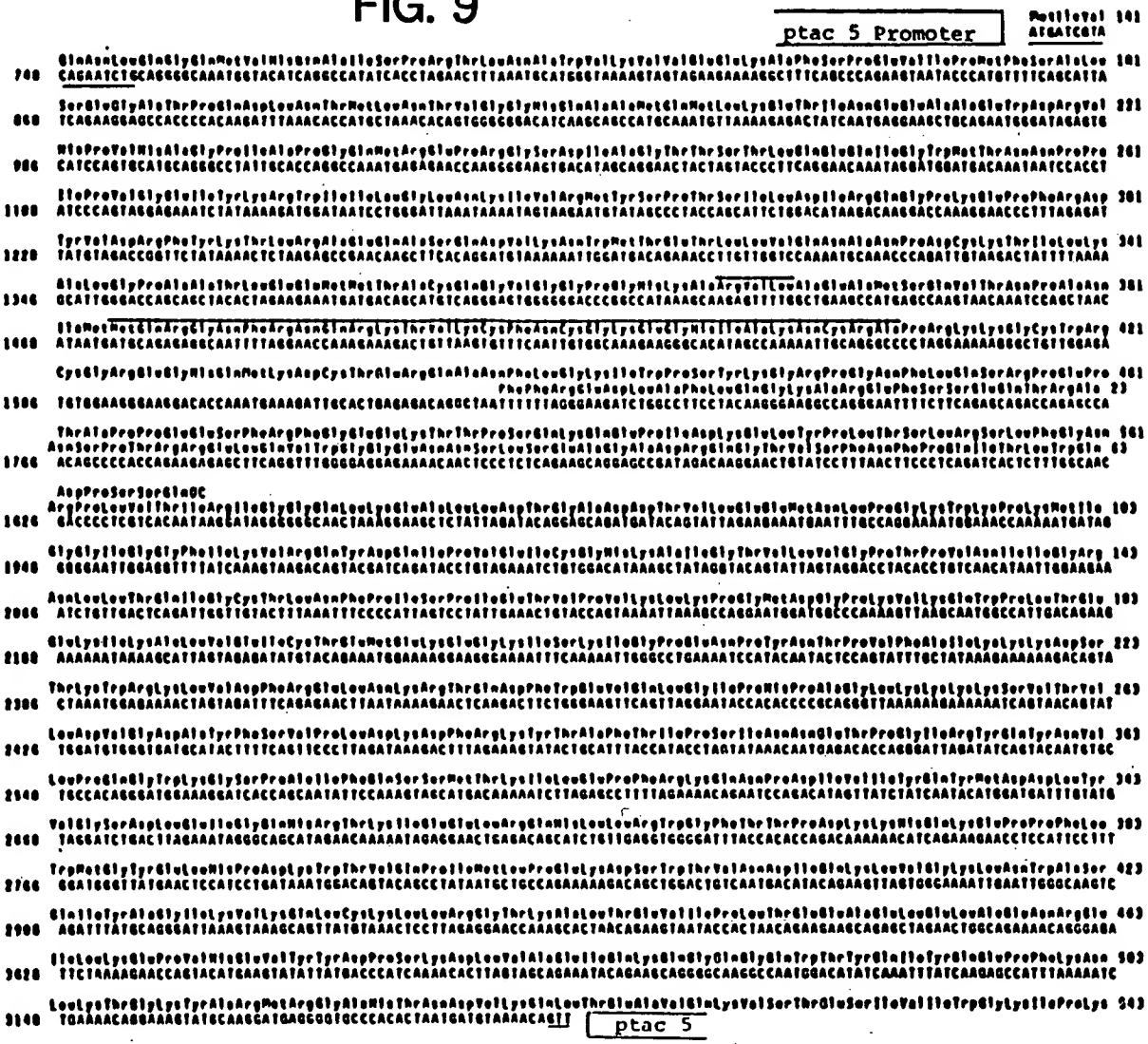
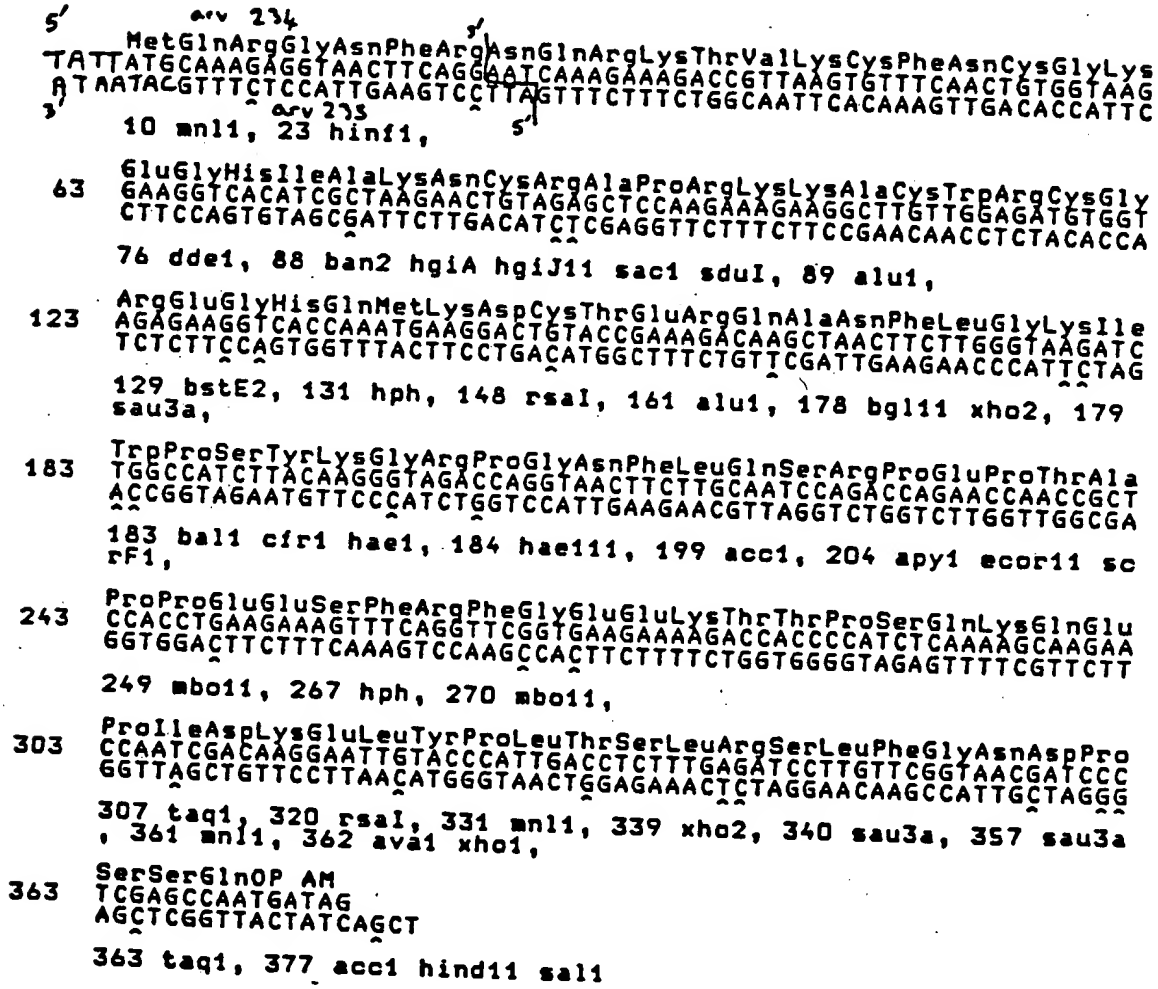


Figure 10

ARV GAG p16 - synthetic Parts A and B



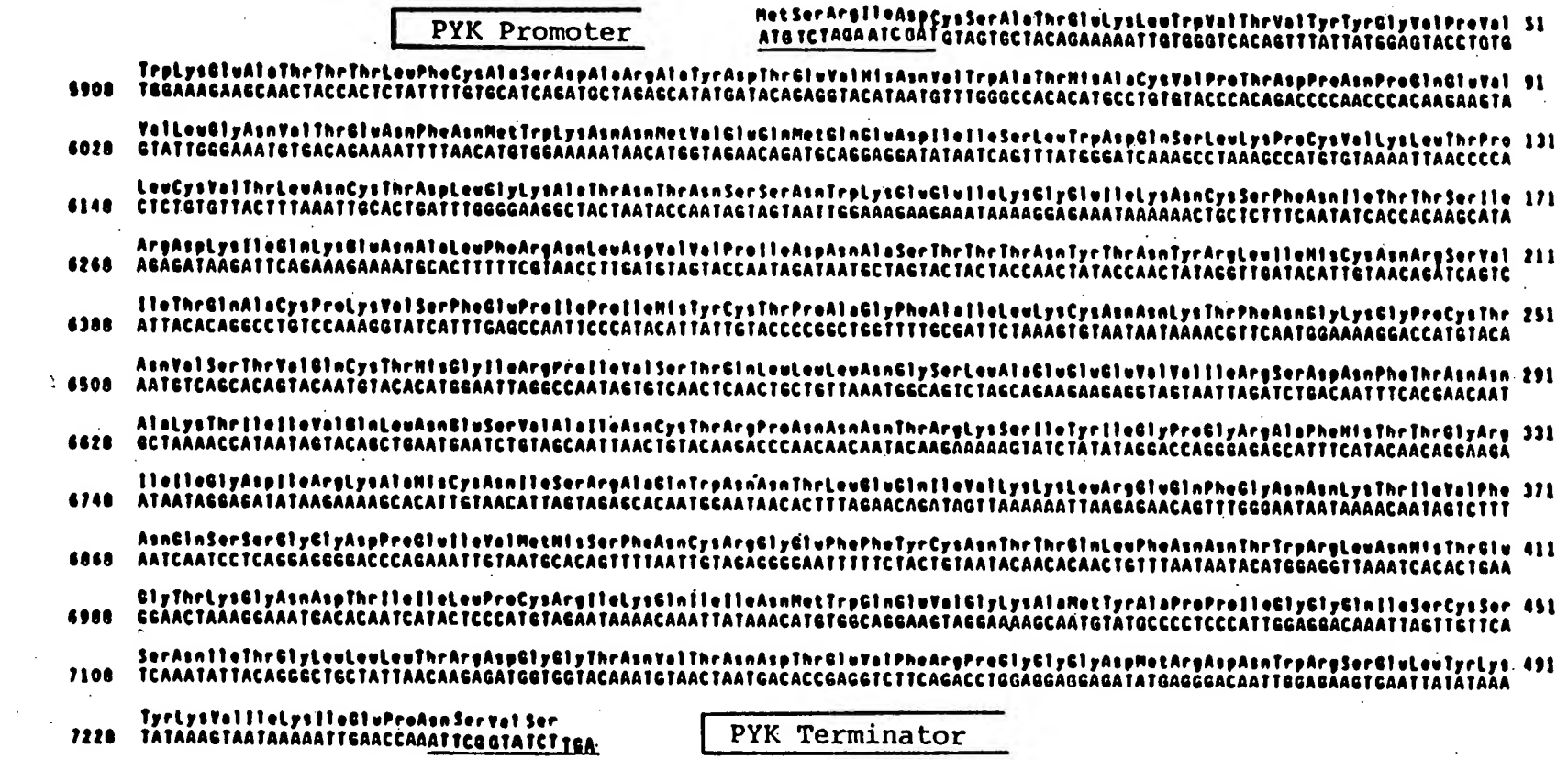


FIG. 11

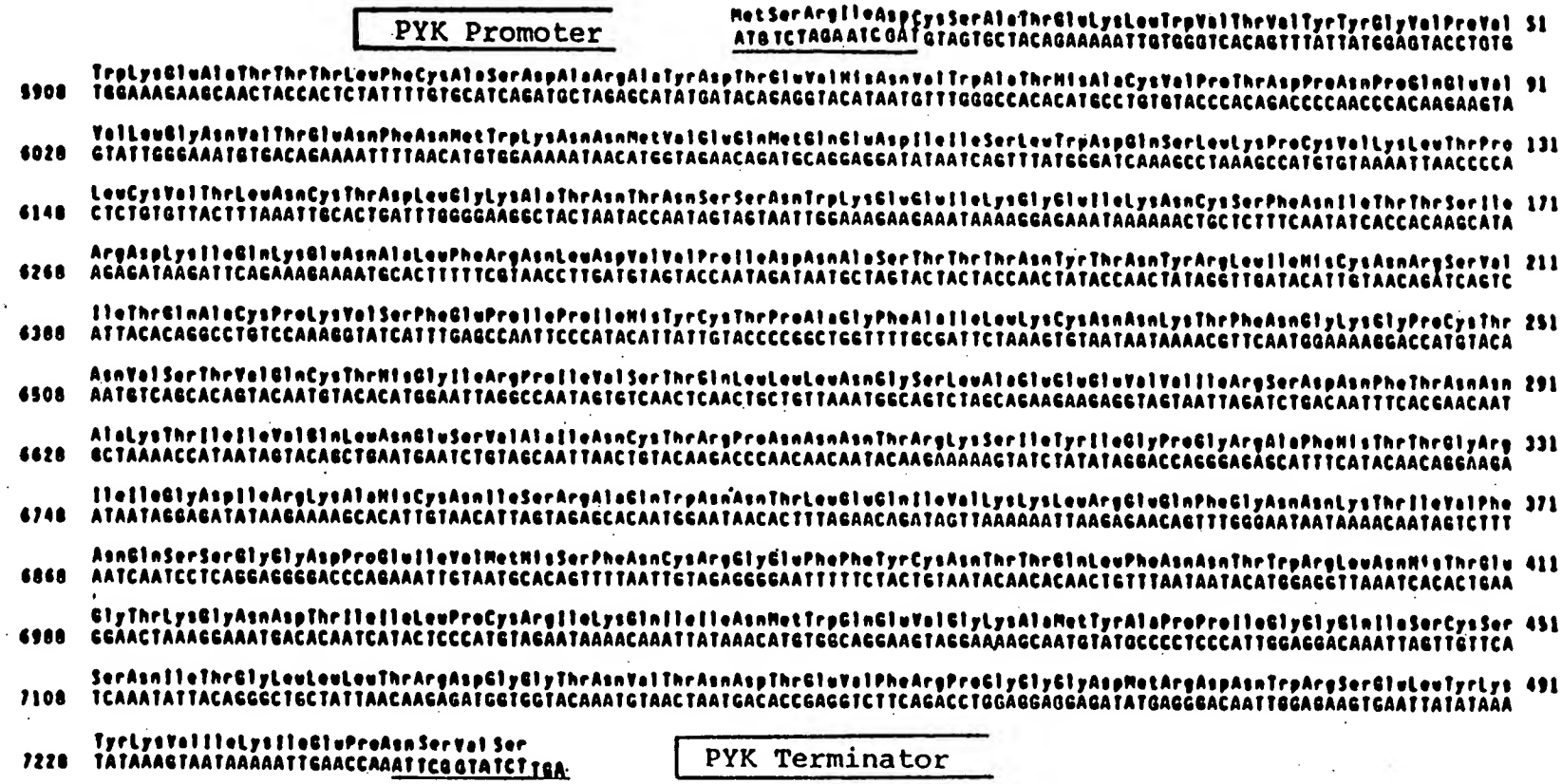


FIG. 11

FIGURE 12

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Nucleotide positions relative to FIGURE 5.

```
                                                MetIleAspLysAlaGlnGluGluHisGluLysTyrHisSerAsnTrp
      1 AGGXAACAG::::ATGAT:GA:AAGGCACAAGAAGAACATGAGAAATATCACAGTAATTGG
        TCCXTTGTC::::TACTA:CT:TTCCGTGTTCTTCTTGTACTCTTTATAGTGTCATTAACC

        32 mbo11, 38 nla111,

        ArgAlaMetAlaSerAspPheAsnLeuProProValValAlaLysGluIleValAlaSer
3820   62 AGAGCCATGGCTAGTGATTTTAACCTGCCACCTGTAGTAGCAAAAGAAATAGTAGCCAGC
        TCTCGGTACCGATCACTAAAATTGGACGGTGGACATCATCGTTTTCTTTATCATCGGTCG

        66 nco1, 67 nla111, 118 nspBII pvu11, 119 alu1,

        CysAspLysCysGlnLeuLysGlyGluAlaMetHisGlyGlnValAspCysSerProGly
3880  122 TGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGTAGACTGTAGTCCAGGA
        ACACTATTTACAGTCGATTTTCCTCTTCGGTACGTACCTGTTCATCTGACATCAGGTCCT

        135 alu1, 151 nla111, 152 nsi1 ava3, 155 nla111, 164 acc1, 1
        76 apy1 bstXI ecor11 scrF1,

        IleTrpGlnLeuAspCysThrHisLeuGluGlyLysIleIleLeuValAlaValHisVal
3940  182 ATATGGCAACTAGATTGTACACATCTAGAAGGAAAAATTATCCTGGTAGCAGTTCATGTA
        TATACCGTTGATCTAACATGTGTAGATCTTCCTTTTTAATAGGACCATCGTCAAGTACAT

        198 rsaI, 205 xba1, 223 apy1 ecor11 scrF1, 236 nla111,

        AlaSerGlyTyrIleGluAlaGluValIleProAlaGluThrGlyGlnGluThrAlaTyr
4000  242 GCCAGTGGATATATAGAAGCAGAAGTTATTCCAGCAGAGACAGGGCAGGAAACAGCATAT
        CGGTCACCTATATATCTTCGTCTTCAATAAGGTCGTCTCTGTCCCGTCCTTTGTCGTATA

        263 xmn1,

        PheLeuLeuLysLeuAlaGlyArgTrpProValLysThrIleHisThrAspAsnGlySer
4060  302 TTTCTCTTAAAATTAGCAGGAAGATGGCCAGTAAAAACAATACATACAGACAATGGCAGC
        AAAGAGAATTTTAATCGTCCTTCTACCGGTCATTTTTGTTATGTATGTCTGTTACCGTCG

        321 mbo11, 326 bal1 cfr1 hae1, 327 hae111, 357 bbv fnu4h1,

        AsnPheThrSerThrThrValLysAlaAlaCysTrpTrpAlaGlyIleLysGlnGluPhe
4120  362 AATTTCACCAGTACTACGGTTAAGGCCGCCTGTTGGTGGGCAGGGATCAAGCAGGAATTT
        TTAAAGTGGTCATGATGCCAATTCCGGCGGACAACCACCCGTCCCTAGTTCGTCCTTAAA

        366 hph, 371 sca1, 372 rsaI, 385 hae111, 386 fnu4h1 nsb11, 4
        05 bin1, 406 dpn1 sau3a,

        GlyIleProTyrAsnProGlnSerGlnGlyValValGluSerMetAsnAsnGluLeuLys
4180  422 GGCATTCCCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCTATGAATAATGAATTAAAG
        CCGTAAGGGATGTTAGGGGTTTCAGTTCCTCATCATCTTAGATACTTATTACTTAATTTC

        423 bsm1, 458 hinf1,

        LysIleIleGlyGlnValArgAspGlnAlaGluHisLeuLysThrAlaValGlnMetAla
4240  482 AAAATTATAGGACAGGTAAGAGATCAGGCTGAACACCTTAAGACAGCAGTACAAATGGCA
        TTTTAATATCCTGTCCATTCTCTAGTCCGACTTGTGGAATTCTGTCGTCATGTTTACCGT

        503 dpn1 sau3a, 518 afl11, 530 rsaI,

        ValPheIleHisAsnPheLysArgLysGlyGlyIleGlyGlyTyrSerAlaGlyGluArg
4300  542 GTATTCATCCACAATTTTAAAAGAAAAGGGGGGATTGGGGGATACAGTGCAGGGGAAAGA
        CATAAGTAGGTGTTAAAATTTTCTTTTCCCCCCTAACCCCCTATGTCACGTCCCCTTTCT

        547 fok1, 557 aha111,

        IleValAspIleIleAlaThrAspIleGlnThrLysGluLeuGlnLysGlnIleThrLys
4360  602 ATAGTAGACATAATAGCAACAGACATACAAACTAAAGAACTACAAAAGCAAATTACAAAA
        TATCATCTGTATTATCGTTGTCTGTATGTTTGATTTCTTGATGTTTTCGTTTAATGTTTT

        605 acc1,

        IleGlnAsnPheArgValTyrTyrArgAspAsnLysAspProLeuTrpLysGlyProAla
      662 ATTCAAAATTTTCGGGTTTATTACAGGGACAACAAAGATCCCCTTTGGAAAGGACCAGCA
```

4480 722 LysLeuLeuTrpLysGlyGluGlyAlaValValIleGlnAspAsnSerAspIleLysVal
AAGCTTCTCTGGAAAGGTGAAGGGGCAGTAGTAATACAAGATAATAGTGACATAAAAGTA
TTCGAAGAGACCTTTCCACTTCCCCGTCATCATTATGTTCTATTATCACTGTATTTTCAT

722 hind111, 723 alu1, 737 hph,

4540 782 ValProArgArgLysAlaLysIleIleArgAspTyrGlyLysGlnMetAlaGlyAspAsp
GTGCCAAGAAGAAAAGCAAAAATCATTAGGGATTATGGAAAACAGATGGCAGGTGATGAT
CACGGTTCTTCTTTTCGTTTTTAGTAATCCCTAATACCTTTTGTCTACCGTCCACTACTA

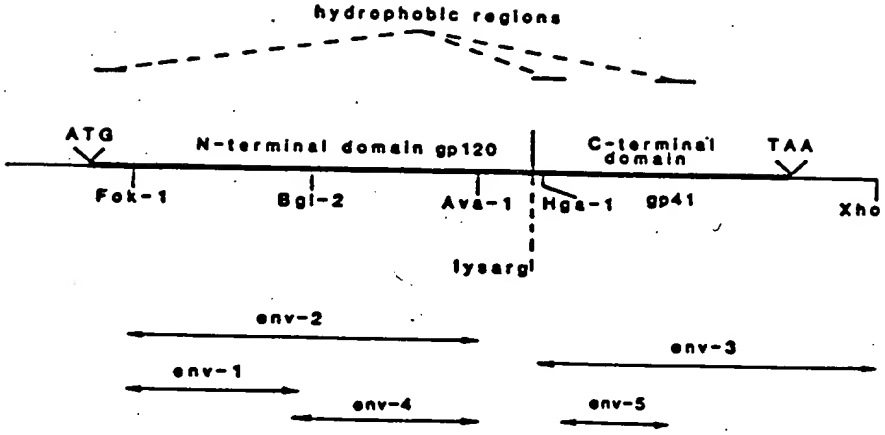
789 mbo11, 833 hph,

4600 842 CysValAlaSerArgGlnAspGluAspAM
TGTGTGGCAAGTAGACAGGATGAGGATTAGTCGACGGAATTCTTTAGTAAAACACC
ACACACCGTTCATCTGTCCTACTCCTAATCAGCTGCCTTAAGAAATCATTTTGTGG

852 acc1, 859 fok1, 863 mnl1, 871 acc1 hind11 sal1, 872 taq1
, 878 ecor1,

FIGURE 12

2 of 2



env expression in yeast and bacteria

FIGURE 13

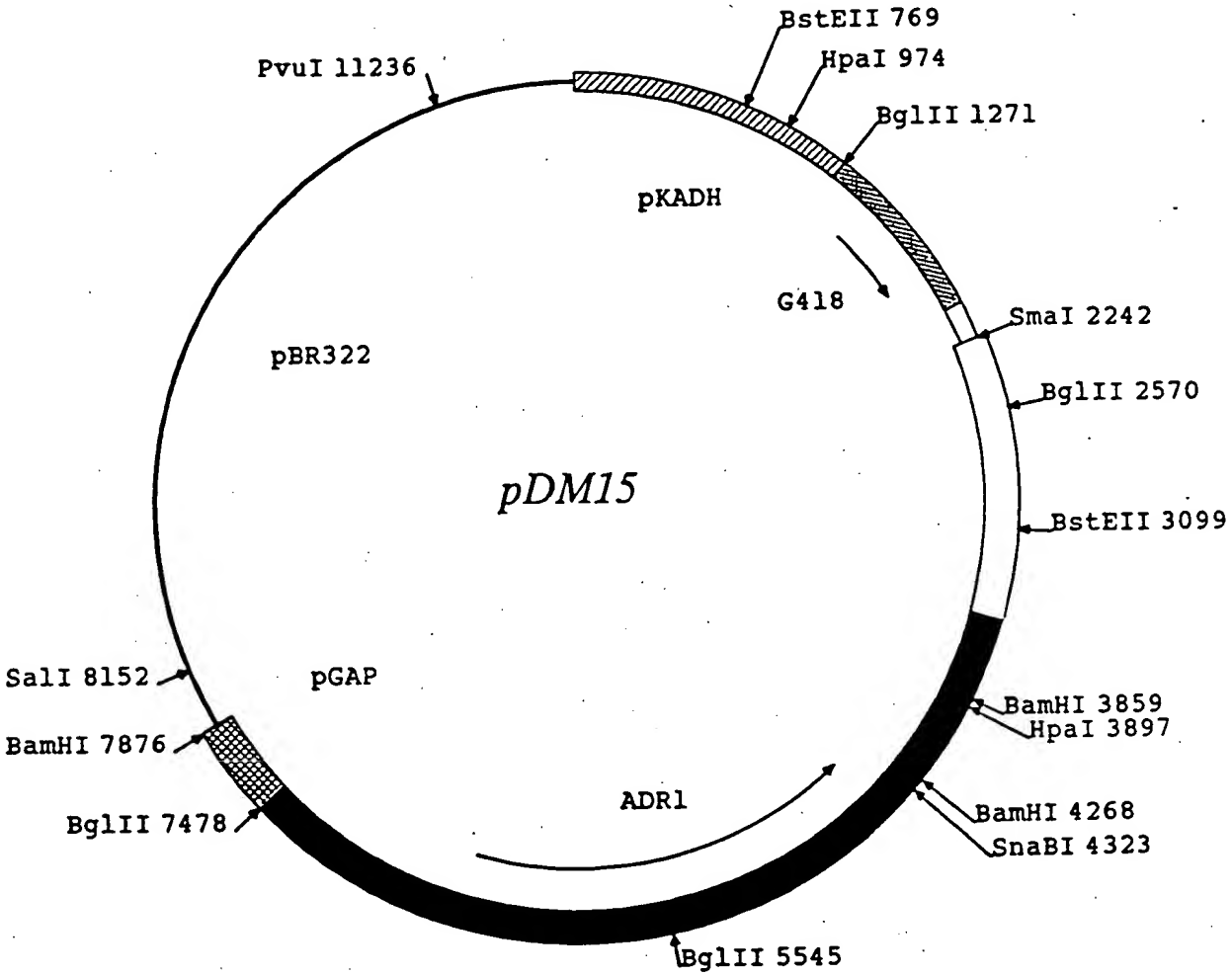


FIGURE 14

SCD

```
    MetAlaThrLysAlaValCysValLeuLysGlyAspGlyProValGlnGlyIleIleAsn
  1 CATGGCGACGAAGGCCGTGTGCGTCTGAAGGGCGACGGCCCAGTGCAGGGCATCATCAAT
    GCTGCTTCCGGCACACGCACGACTTCCCGCTGCCGGGTCACGTCCCGTAGTAGTTA

    PheGluGlnLysGluSerAsnGlyProValLysValTrpGlySerIleLysGlyLeuThr
 62 TTCGAGCAGAAGGAAAGTAATGGACCAGTGAAGGTGTGGGGAAGCATTAAAGGACTGACT
    AAGCTCGTCTTCCTTTCATTACCTGGTCACTTCCACACCCCTTCGTAATTTCCTGACTGA

    GluGlyLeuHisGlyPheHisValHisGluPheGlyAspAsnThrAlaGlyCysThrSer
122 GAAGGCCTGCATGGATTCCATGTTCATGAGTTTGGAGATAATACAGCAGGCTGTACCAGT
    CTTCCGGACGTACCTAAGGTACAAGTACTCAAACCTCTATTATGTCGTCCGACATGGTCA

    AlaGlyProHisPheAsnProLeuSerArgLysHisGlyGlyProLysAspGluGluArg
182 GCAGGTCCTCACTTTAATCCTCTATCCAGAAAACACGGTGGGCCAAAGGATGAAGAGAGG
    CGTCCAGGAGTGAAATTAGGAGATAGGTCTTTTGTGCCACCCGGTTTCCTACTTCTCTCC

    HisValGlyAspLeuGlyAsnValThrAlaAspLysAspGlyValAlaAspValSerIle
242 CATGTTGGAGACTTGGGCAATGTGACTGCTGACAAAGATGGTGTGGCCGATGTGTCTATT
    GTACAACCTCTGAACCCGTTACACTGACGACTGTTTCTACCACACCGGCTACACAGATAA

    GluAspSerValIleSerLeuSerGlyAspHisCysIleIleGlyArgThrLeuValVal
302 GAAGATTCTGTGATCTCACTCTCAGGAGACCATTGCATCATTGGCCGCACACTGGTGGTC
    CTTCTAAGACACTAGAGTGAGAGTCCTCTGGTAACGTAGTAACCGGCGTGTGACCACCAG

    HisGluLysAlaAspAspLeuGlyLysGlyGlyAsnGluGluSerThrLysThrGlyAsn
362 CATGAAAAAGCAGATGACTTGGGCAAAGGTGGAAATGAAGAAAGTACAAAGACAGGAAAC
    GTACTTTTTCGTCTACTGAACCCGTTTCCACCTTTACTTCTTTCATGTTTCTGTCCTTTG

                                                    ENV 5B
    AlaGlySerArgLeuAlaCysGlyValIleGlyIleAlaMetAlaIleGluAlaGlnGln
422 GCTGGAAGTCGTTTGGCTTGTGGTGTAATTGGGATCGCCATGGCTATCGAAGCTCAACAA
    CGACCTTCAGCAAACCGAACACCACATTAACCCTAGCGGTACCGATAGCTTCGAGTTGTT
                                                    401

    HisLeuLeuGlnLeuThrValTrpGlyIleLysGlnLeuGlnAlaArgValLeuAlaVal
482 CACTTGCTGCAGTTGACCGTTTGGGGTATCAAGCAGTTGCAGGCTAGAGTTTTGGCTGTT
    GTGAACGACGTCAACTGGCAAACCCCATAGTTCGTCAACGTCCGATCTCAAAACCGACAA

    GluArgTyrLeuArgAspGlnGlnLeuLeuGlyIleTrpGlyCysSerGlyLysLeuIle
542 GAAAGATACTTGAGAGATCAACAATTGTTGGGTATCTGGGGTTGTTCTGGTAAGTTGATT
    CTTTCTATGAACTCTCTAGTTGTTAACAACCCATAGACCCCAACAAGACCATTCAACTAA

    CysThrThrAlaValProTrpAsnAlaSerTrpSerAsnLysSerLeuGluAspIleTrp
602 TGTACCACCGCTGTTCCCTGGAACGCTTCTTGGTCTAACAAGTCTTTGGAAGACATCTGG
    ACATGGTGGCGACAAGGGACCTTGCGAAGAACCAGATTGTTCAGAAACCTTCTGTAGACC

    AspAsnMetThrTrpMetGlnTrpGluArgGluIleAspAsnTyrThrAsnThrIleTyr
662 GACAACATGACCTGGATGCAATGGGAAAGAGAAATCGACAACTACACCAACACCATCTAC
    CTGTTGTACTGGACCTACGTTACCCTTTCTCTTTAGCTGTTGATGTGGTTGTGGTAGATG

    ThrLeuLeuGluGluSerGlnAsnGlnGlnGluLysAsnGluGlnGluLeuLeuGluLeu
722 ACCTTGTTGGAGGAATCTCAAAACCAACAAGAAAAGAACGAACAAGAATTGTTGGAATTG
    TGGAACAACCTCCTTAGAGTTTTGGTTGTTCTTTTCTTGCTTGTTCTTAACAACCTTAAC

    AspLysTrpAlaSerLeuTrpAsnTrpPheSerIleThrAsnTrpAM
782 GACAAGTGGGCAAGCTTGTGGAACTGGTTCTCTATCACCAACTGGTAG
    CTGTTCACCCGTTCGAACACCTTGACCAAGAGATAGTGGTTGACCATCAGCT
```

Translated Mol. Weight = 30414.22

FIGURE 15

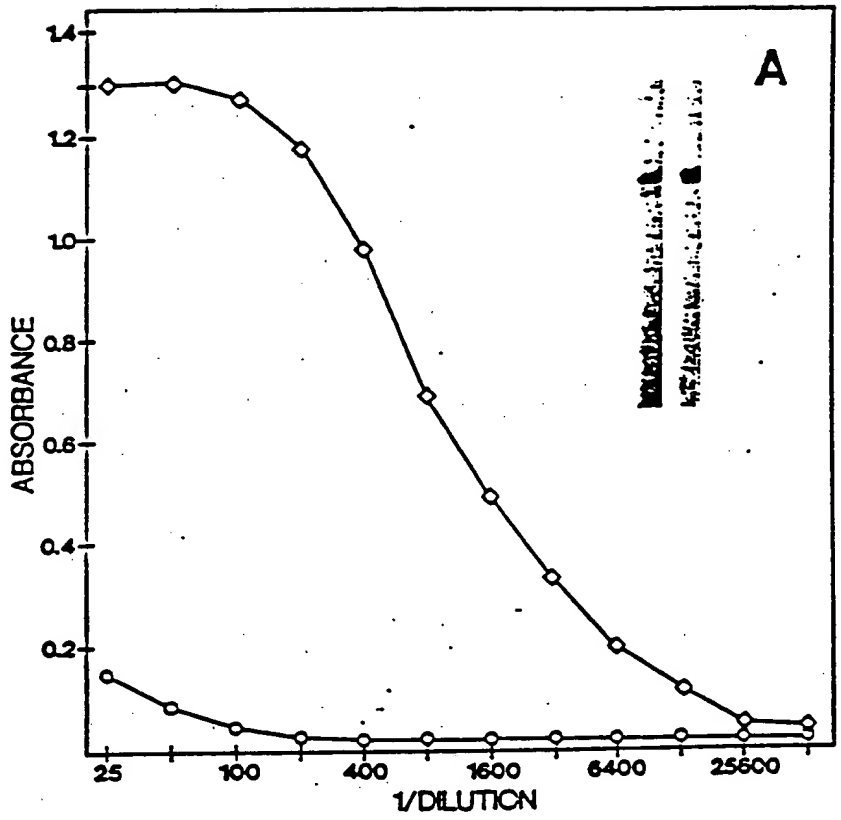

A
ABSORBANCE
1.4
1.2
1.0
0.8
0.6
0.4
0.2
25
100
400
1600
6400
25600
1/DILUTION

FIGURE 16

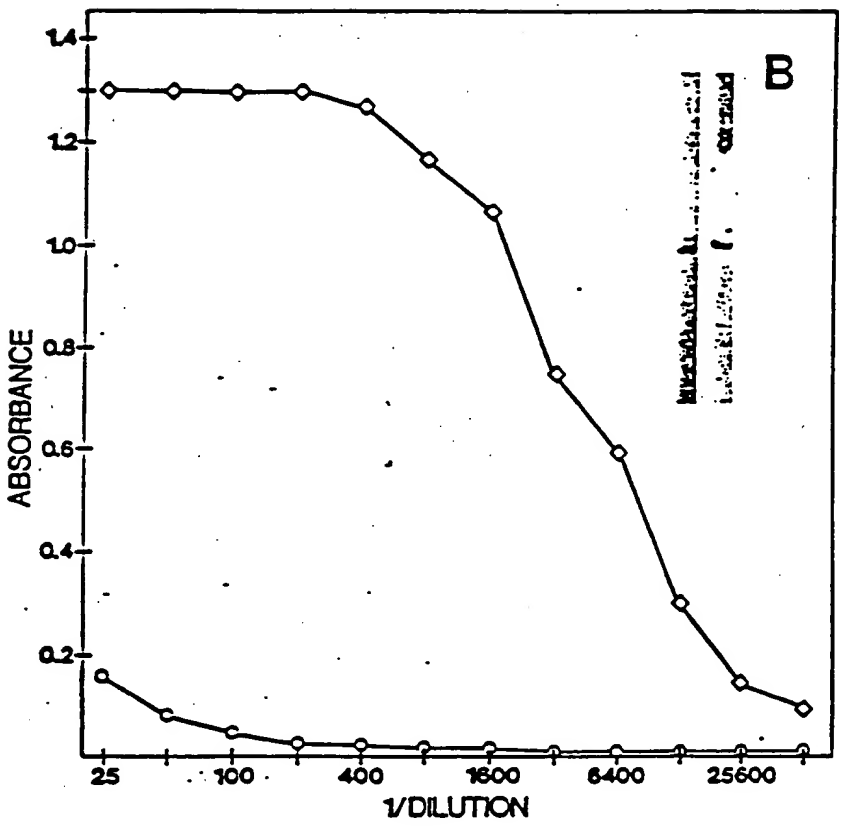


FIGURE 16

2 of 2

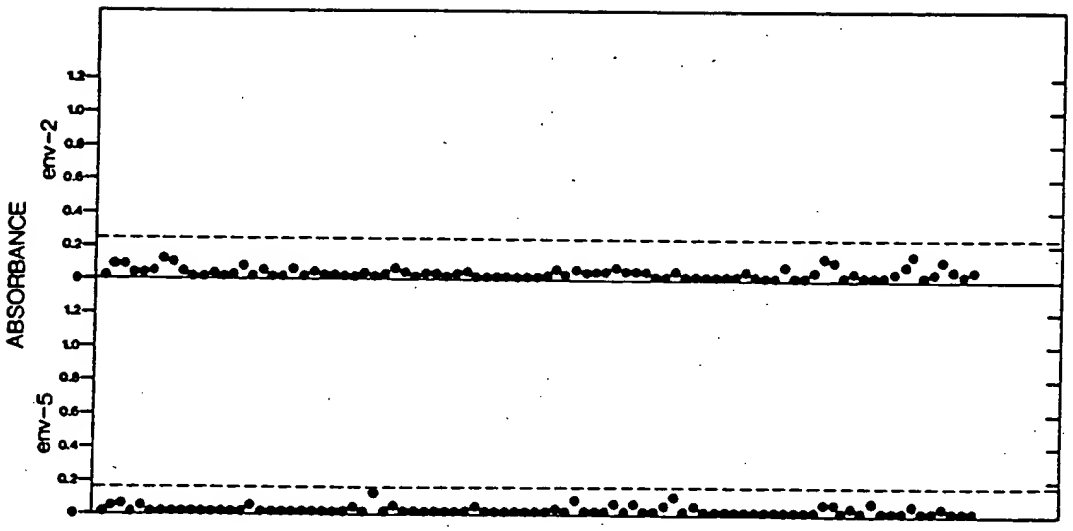


FIGURE 17

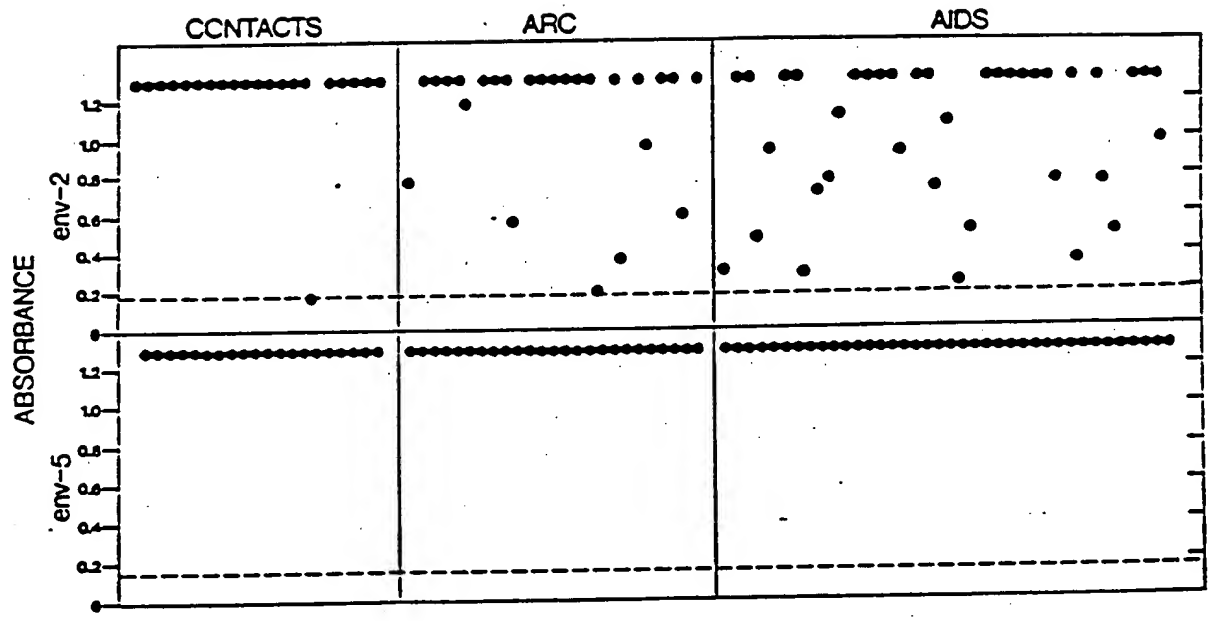


FIGURE 18

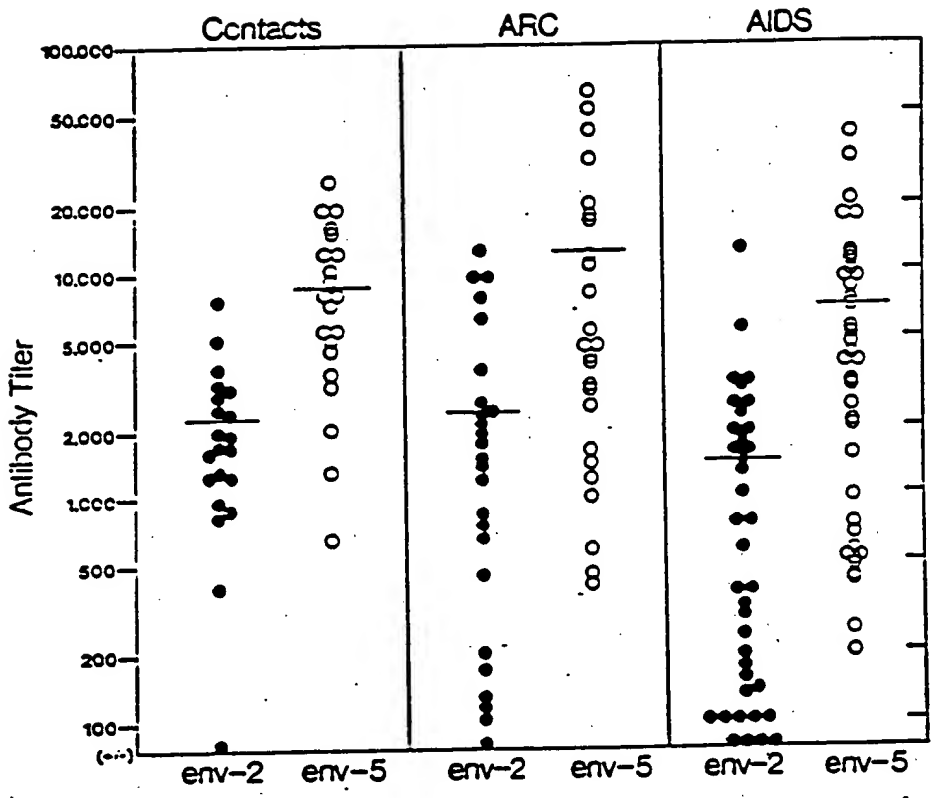
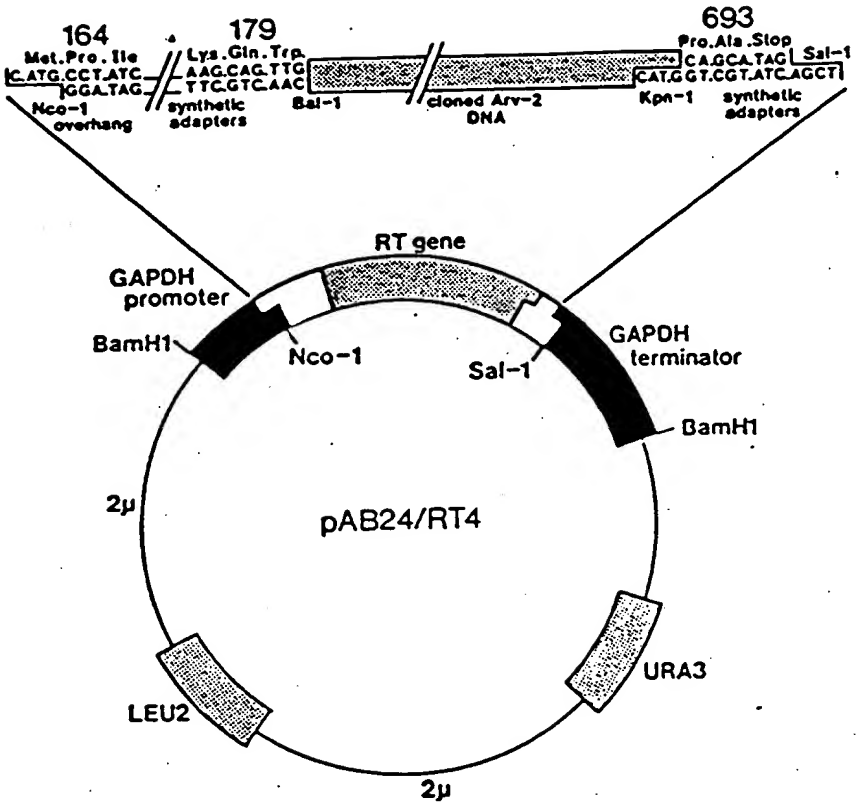


FIGURE 19



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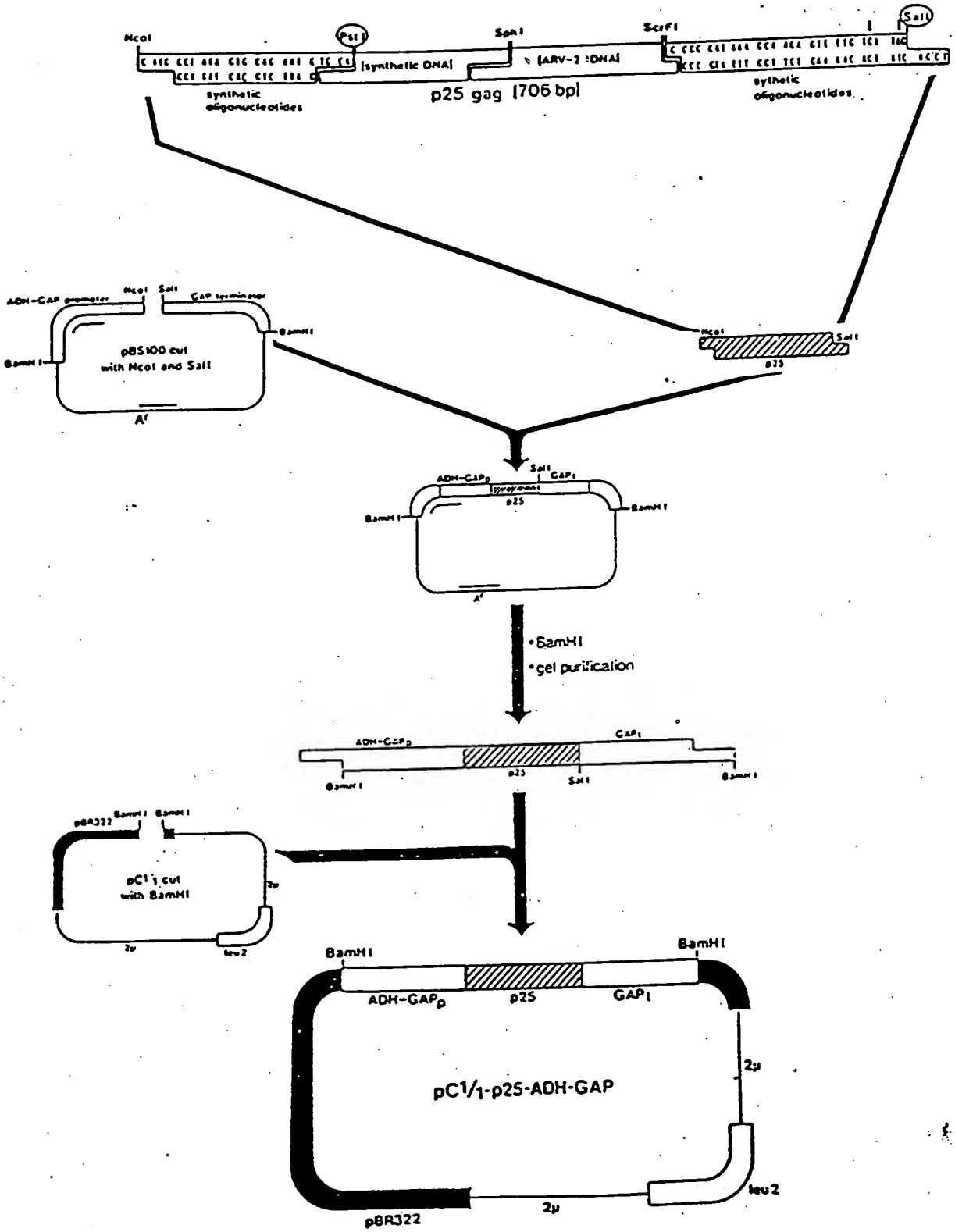

FIGURE 21

```
     1                                                  10
     Met Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln
C    ATG CCT ATA GTG CAG AAT CTG CAG GGG CAA ATG GTA CAT CAG

                    20
Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
GCC ATA TCA CCT AGA ACT TTA AAT GCT TGG GTA AAA GTA GTA GAA

 30                                                 40
Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
GAA AAG GCT TTC AGC CCA GAA GTA ATA CCC ATG TTT TCA GCA TTA

                    50
Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
TCA GAA GGA GCC ACC CCT CAA GAT TTA AAC ACC ATG CTA AAC ACA

 60                                                 70
Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile
GTG GGG GGA CAT CAA GCA GCC ATG CAA ATG TTA AAA GAG ACT ATC

                    80
Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala
AAT GAG GAG GCT GCC GAA TGG GAT AGA GTG CAT CCA GTG CAT GCA

 90                                                100
Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp
GGG CCT ATT GCA CCA GGC CAA ATG AGA GAA CCA AGG GGA AGT GAC

                   110
Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
ATA GCA GGA ACT ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG

120                                                130
Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp
ACA AAT AAT CCA CCT ATC CCA GTA GGA GAA ATC TAT AAA AGA TGG

                   140
Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr
ATA ATC CTG GGA TTA AAT AAA ATA GTA AGA ATG TAT AGC CCT ACC

150                                                160
Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp
AGC ATT CTG GAC ATA AGA CAA GGA CCA AAG GAA CCC TTT AGA GAT

                   170
Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser
TAT GTA GAC CGG TTC TAT AAA ACT CTA AGA GCC GAA CAA GCT TCA

180                                                190
Gln Asp Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn
CAG GAT GTA AAA AAT TGG ATG ACA GAA ACC TTG TTG GTC CAA AAT

                   200
Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala
GCA AAC CCA GAT TGT AAG ACT ATT TTA AAA GCA TTG GGA CCA GCA

210                                                220
Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
GCT ACA CTA GAA GAA ATG ATG ACA GCA TGT CAG GGA GTG GGG GGA

                   230     232
Pro Gly His Lys Ala Arg Val Leu OP
CCC GGG CAT AAA GCA AGA GTT TTG TGA TAG

Translated Mol. Weight = 25700.75
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FIGURE 22

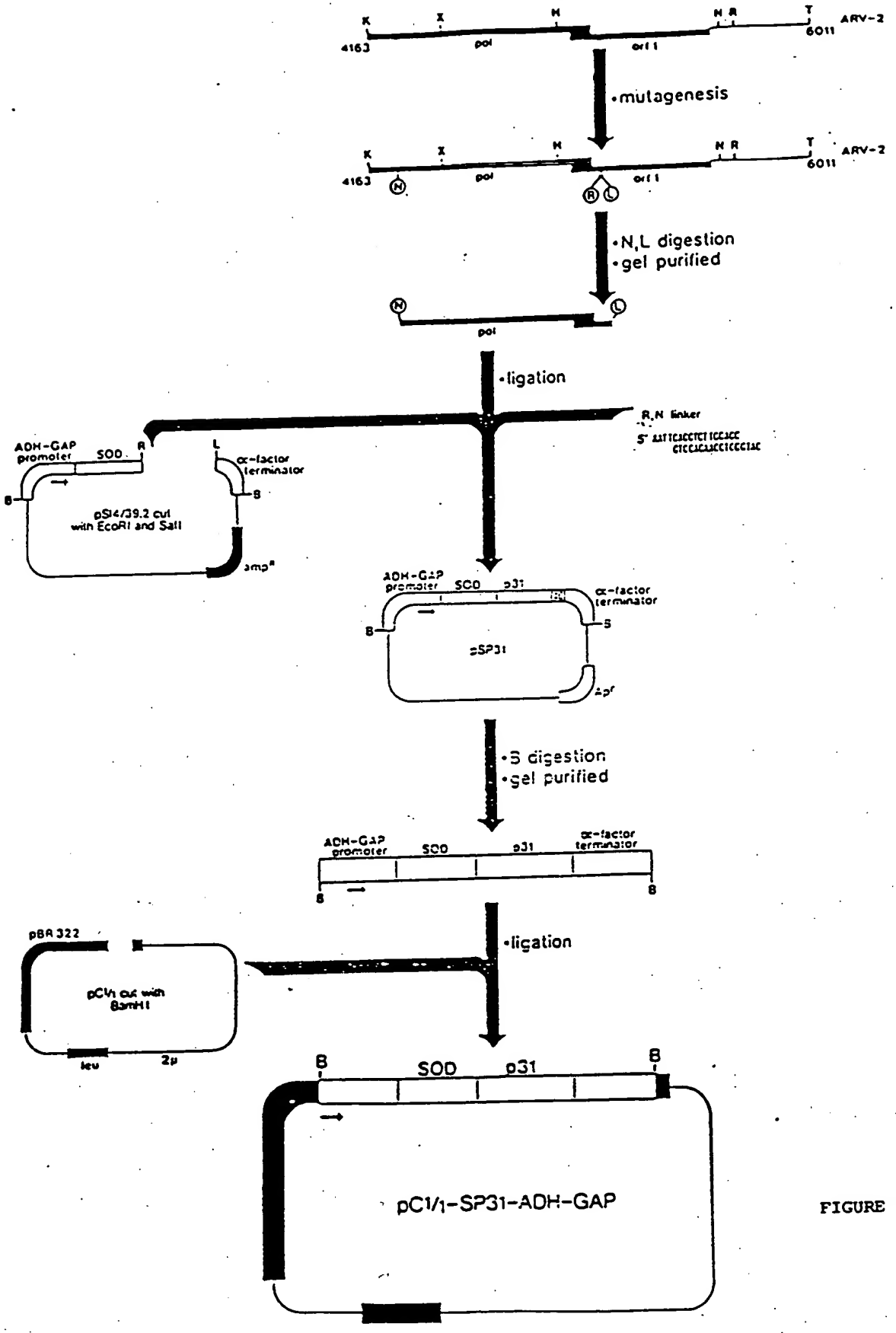


FIGURE 23

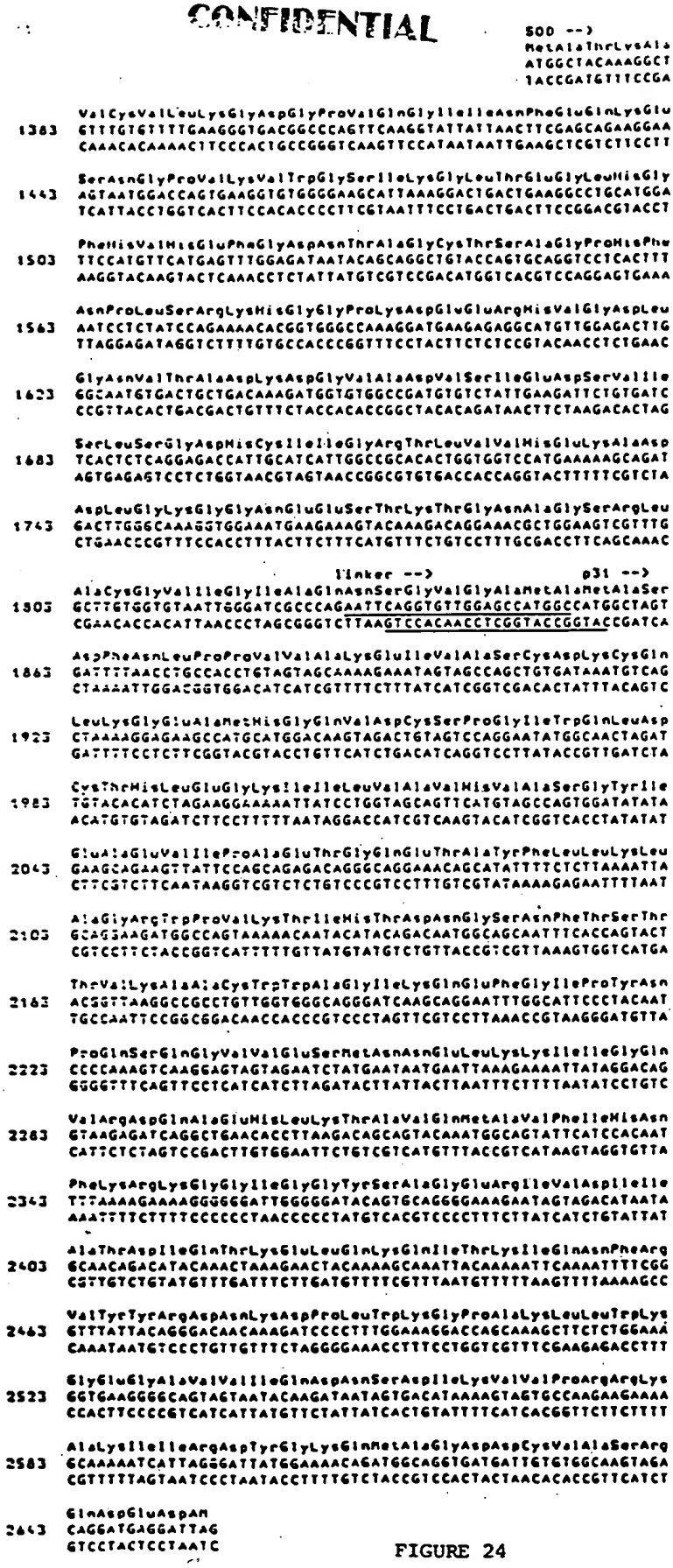


FIGURE 24

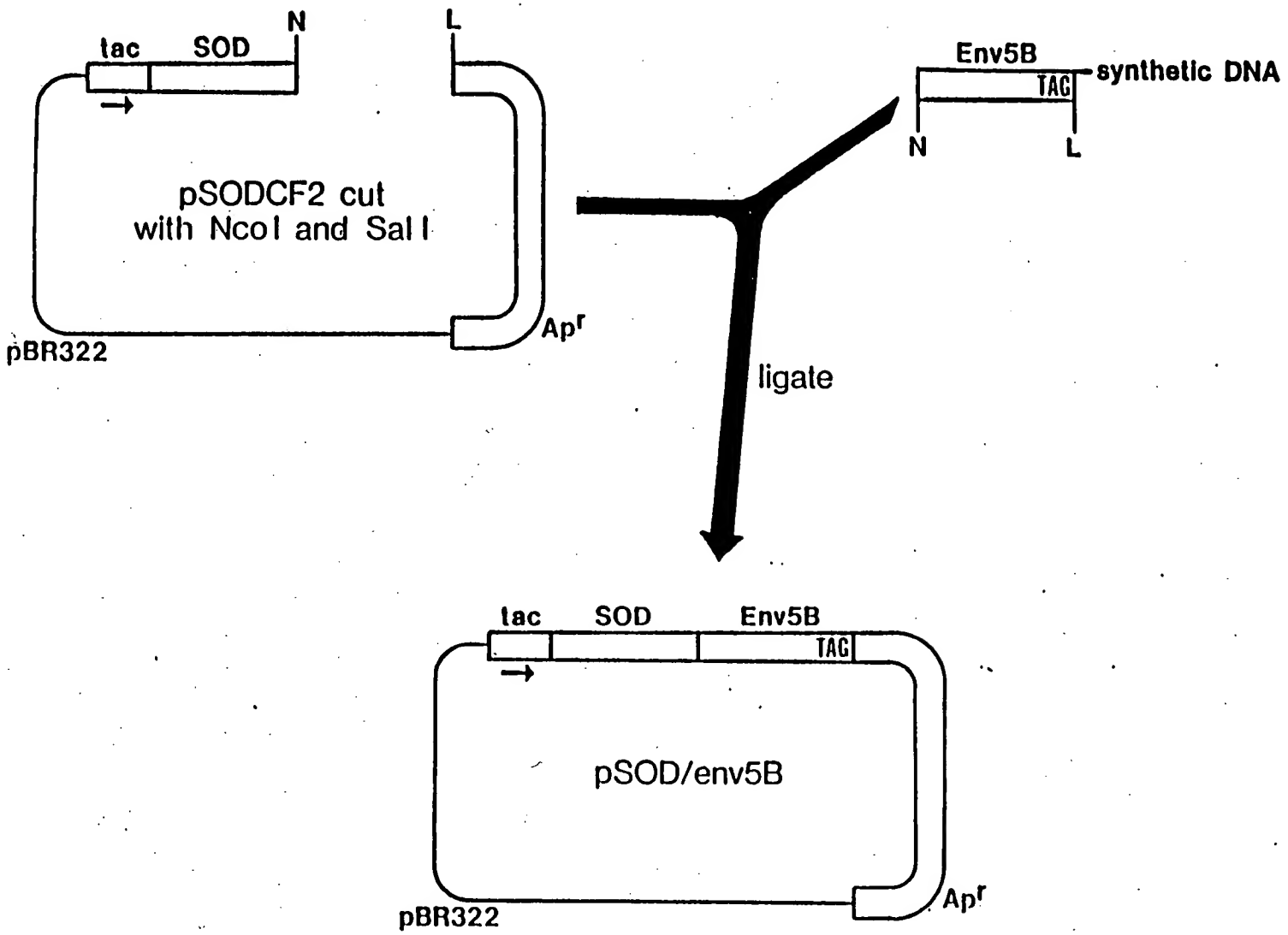
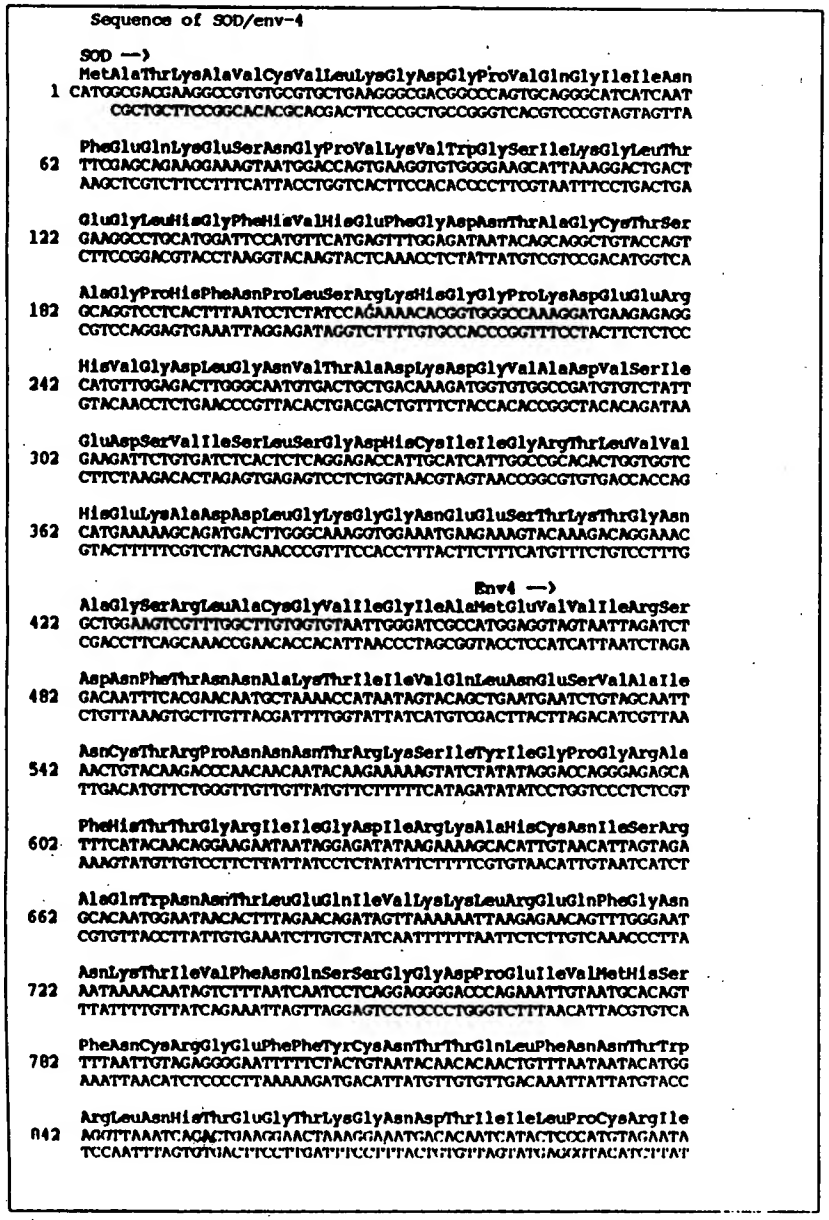
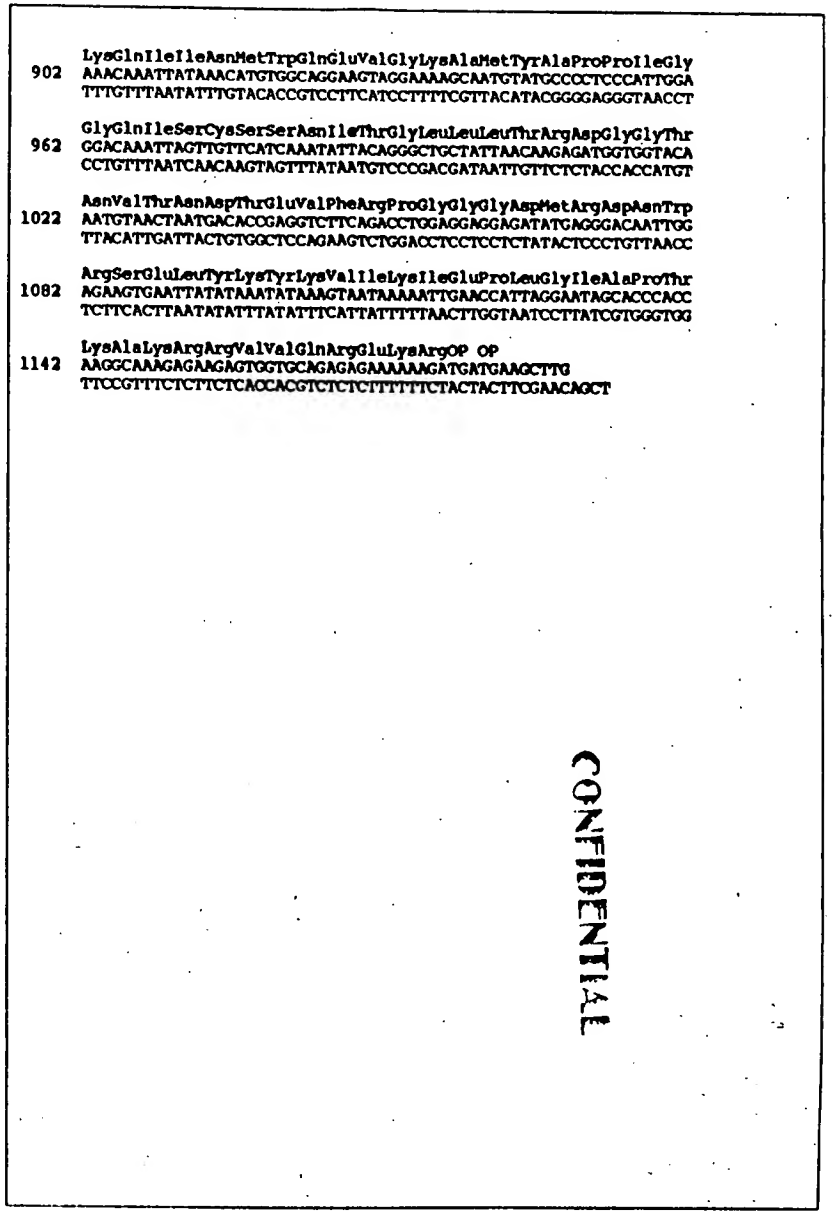


FIGURE 25

FIGURE 26





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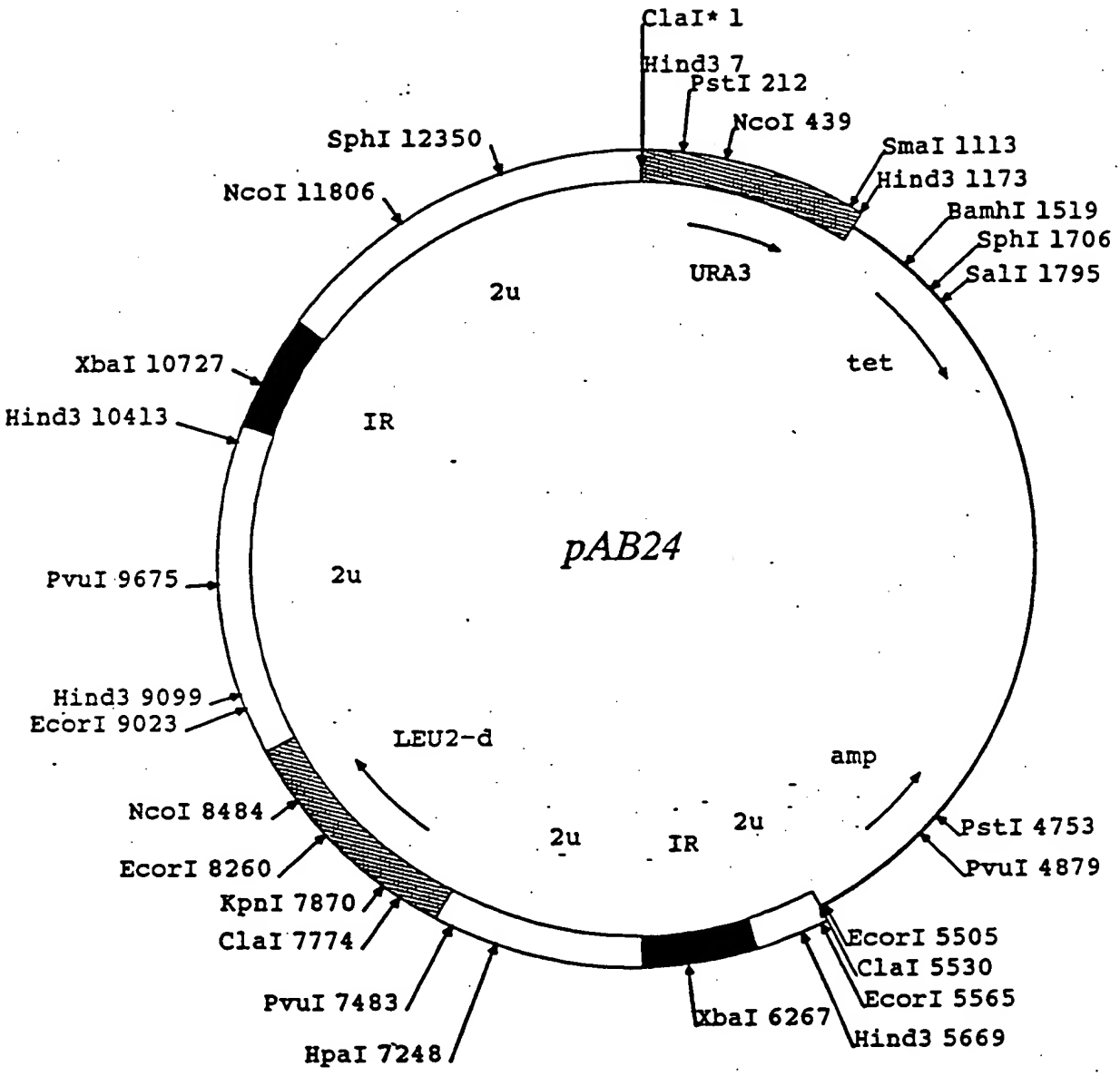

FIGURE 27

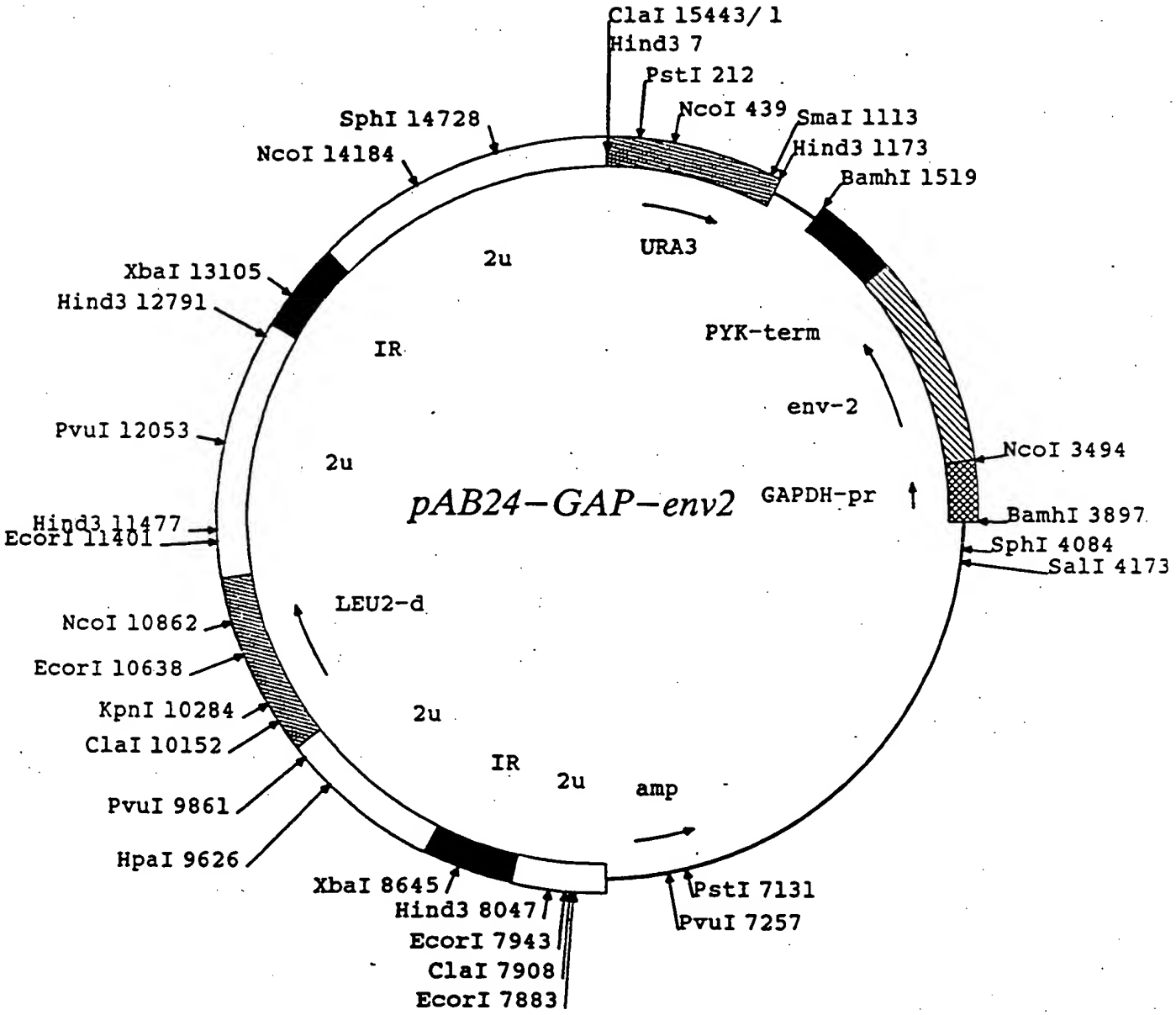

FIGURE 28

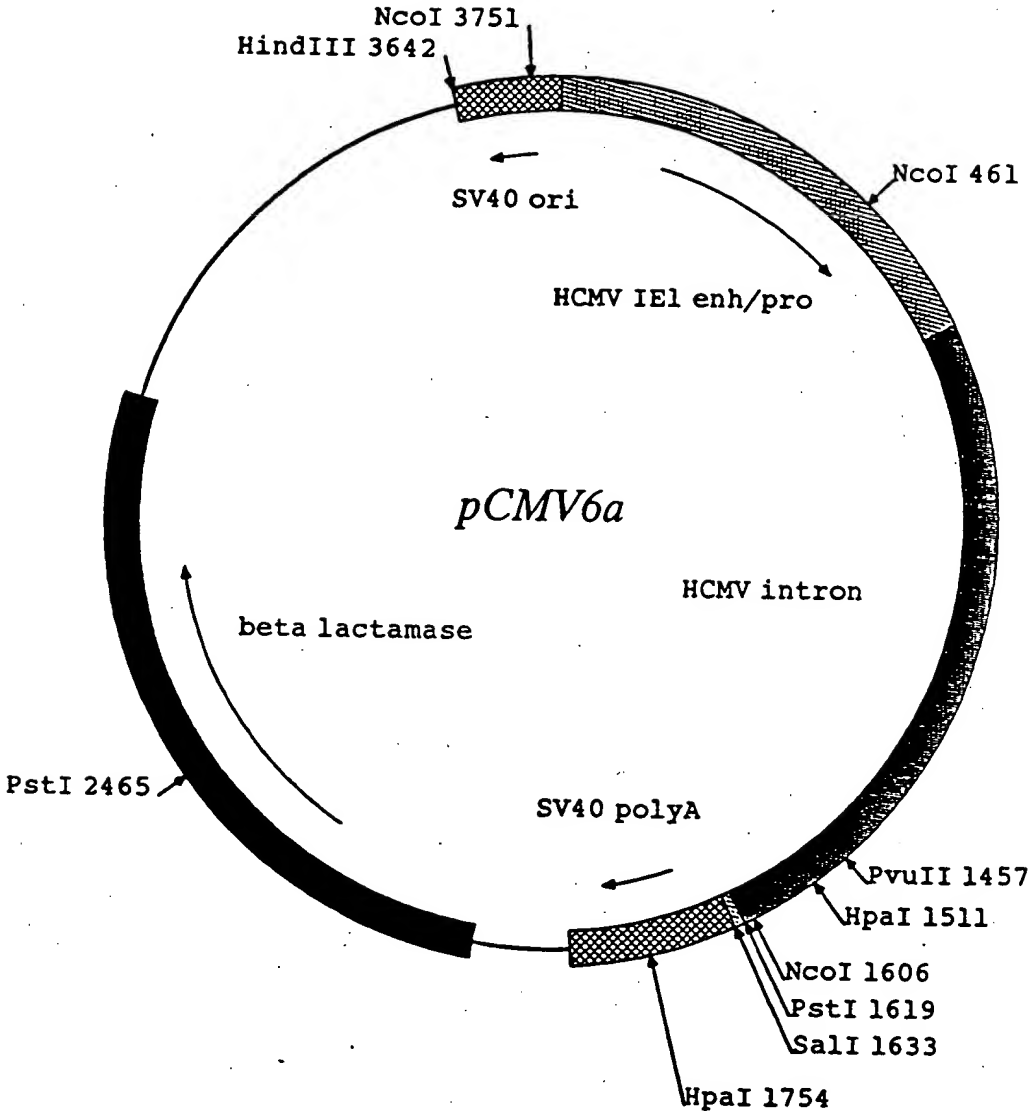

FIGURE 29

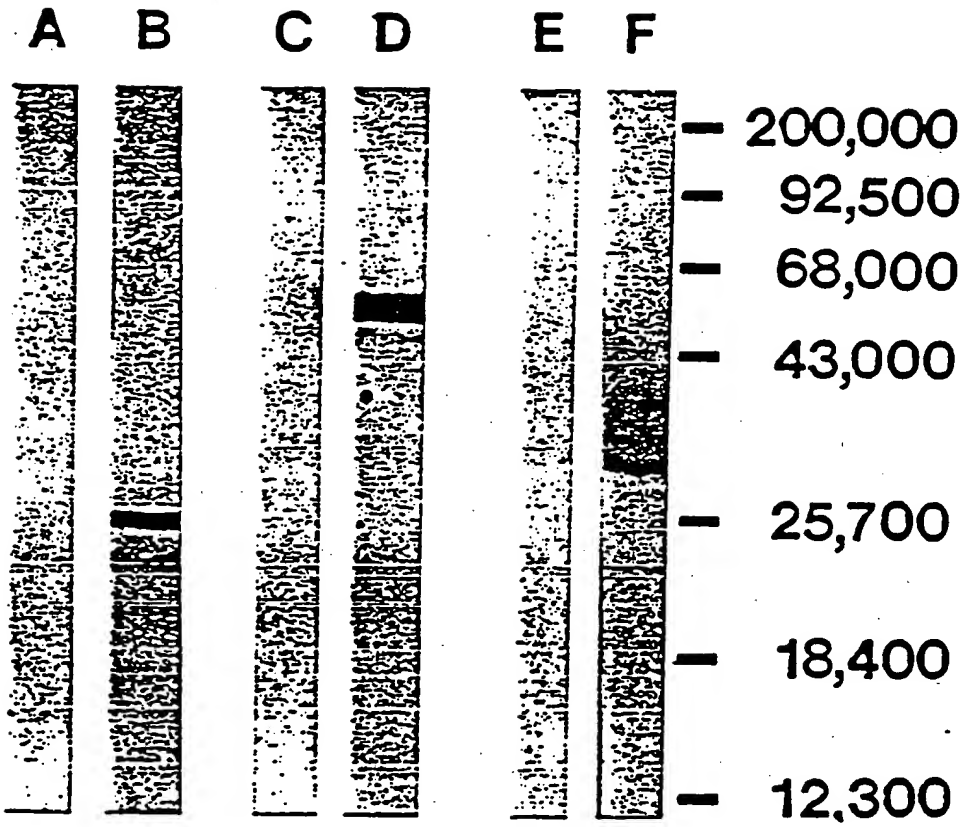

FIGURE 30